

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 15:59:43 ; Search time 1229 Seconds
(without alignments)
7104.021 Million cell updates/sec

Title: US-09-721-391-1

Perfect score: 300

Sequence: 1 tcatttgcaaggtcaaatca.....agccaagacatgtgataatc 300

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_on.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

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26: em_ro.*

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28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

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35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chagne to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	300	100.0	300	6	AX269131	AX269131 Sequence
2	300	100.0	1629	9	HUMTYR01	M3235 Human tyros
3	300	100.0	2384	6	AR167367	AR167367 Sequence
4	300	100.0	2384	6	E11466	E11466 cDNA encodi
5	300	100.0	2384	6	I49609	I49609 Sequence 1
6	300	100.0	2384	9	HUMTYR01	M2160 Human tyros
7	300	100.0	3586	9	HSTYR01E	X16073 Human tyros
8	300	100.0	147357	9	AP000720	AP000720 Homo sapi
9	293.6	97.9	1563	9	PAPATYR1	AF183649 Pan panis
10	292	97.3	1563	9	PTTYR1	AF183588 Pan trogl
11	289	96.3	2311	9	HS005039	U03034 Human tyros
12	289	96.3	2397	6	I70158	I70158 Sequence 11
13	287.2	95.7	1557	9	MNTYR1	AF183578 Macaca ne
14	287.2	95.7	1558	9	COPTYR1	AF183593 Colobus p
15	287.2	95.7	1558	9	MATYR1	AF183614 Macaca ar
16	287.2	95.7	1558	9	MAASTYR1	AF183619 Macaca as
17	287.2	95.7	1559	9	MAFATYR1	AF183624 Macaca fa
18	287.2	95.7	1560	9	MAMUTYR1	AF183629 Macaca mu
19	287.2	95.7	1560	9	MTYR1	AF183659 Macaca th
20	285.6	95.2	1441	9	PHYTYR1	AF183683 Papio ham
21	285.6	95.2	1556	9	PNTYR1	AF183654 Pygathrix
22	274.2	91.4	1562	9	RRTYR1	AF183669 Rhinopith
23	272.8	90.9	1563	9	HHTYR1	AF183604 Hylobates
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25	272.6	90.9	1560	9	PBTYR1	AF183684 Pygathrix
26	272.6	90.9	1563	9	TRFRTYR1	AF183674 Trachypit
27	272	90.7	1561	9	TPTYR1	AF183664 Trachypit
28	269.6	89.9	1561	9	HLTYP1	AF183609 Hylobates
29	267.8	89.3	1560	9	TLTYR1	AF183679 Trachypit
30	266	88.7	1554	9	NLTYP1	AF183639 Nasalis 1
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32	235	78.3	3586	6	AX339194	AX339194 Sequence
33	229.6	76.5	1510	9	APTYR1	AF187155 Ateles pa
34	219	73.0	546	6	AX259950	AX259950 Sequence
35	219	73.0	546	6	AX262355	AX262355 Sequence
36	202.4	67.5	3586	6	AX339195	AX339195 Sequence
37	149.2	49.7	1169	9	GOGOTYR2	AF183599 Gorilla g
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42	68.6	22.9	5505	2	AL831717	AI831717 Mus muscu
43	68.6	22.9	179598	2	AC084321	AC084321 Mus muscu
44	68.6	22.9	230967	2	AC122517	AC122517 Mus muscu
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ALIGNMENTS

RESULT 1
AX269131
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE

AX269131
Sequence 2 from Patent WO0174861.
AX269131
AX269131.1 GI:16542051
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
1
Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.
Compositions and methods for tissue specific gene regulation
therapy

AX269131
Sequence 2 from Patent WO0174861.
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AX269131.1 GI:16542051
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
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Sequence 2 from Patent WO0174861.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
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1
Ville, R.G., Harrington, K., Murphy, S. and Bateman, A.
Compositions and methods for tissue specific gene regulation
therapy

JOURNAL Patent: WO 0174861-A 2 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
FEATURES Location/Qualifiers
source 1..300
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 95 a 43 c 63 g 99 t
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Best Local Similarity 100.0%; Pred. No. 1e-57;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 300
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Db 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 300
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RESULT 2
HUMTYR01
LOCUS HUMTYR01 1629 bp DNA linear PRI 14-JAN-1995
DEFINITION Human tyrosinase gene, exon 1.
ACCESSION M63235 M60296
VERSION M63235.1 GI:340029
KEYWORDS tyrosinase.
SEGMENT 1 of 5
SOURCE Human DNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
Gibbel, L.B., Strunk, K.M. and Spritz, R.A.
Organization and nucleotide sequences of the human tyrosinase gene
and a truncated tyrosinase-related segment
Genomics 9 (3), 435-445 (1991)
JOURNAL 91236163
MEDLINE 1903356
PUBMED
FEATURES Location/Qualifiers
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/map="llq14-q21"
590..1488
/note="minor 5' mRNA terminus"
/number=1
/evidence=experimental
595..1488
/note="minor 5' mRNA terminus"
/number=1
/evidence=experimental
624..1488
/note="major 5' mRNA terminus"
/number=1
/evidence=experimental
670..723
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/note="G00-120-476"

exon
exon
exon
sig_peptide

BASE COUNT 469 a 342 c 353 g 465 t
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Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 GGTGAATAGAGTTTTTCACTTTAATACATAGGCTATCCACCTGGTGGGATACGAGCCCAATT 180
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Qy 181 CGAAGAAAGTCAGTCATGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Db 471 CGAAGAAAGTCAGTCATGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 530
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Qy 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 300
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Db 531 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 590
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RESULT 3
AR167367
LOCUS AR167367 2384 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6287569.
ACCESSION AR167367
VERSION AR167367.1 GI:17903142
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2384)
AUTHORS Kipps, T.J. and Wu, Y.
TITLE Vaccines with enhanced intracellular processing
JOURNAL Patent: US 6287569-A 3 11-SEP-2001;
FEATURES Location/Qualifiers
source 1..2384
/organism="unknown"
BASE COUNT 652 a 533 c 520 g 679 t
ORIGIN

Query Match 100.0%; Score 300; DB 6; Length 2384;
Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATTGCAAGGTCAAAATCATCTAGTTTGTAGTCTATTAACTGGGTTTGCCTTAGGTC 60
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Qy 121 GGTGAATAGAGTTTTTCACTTTAATACATAGGCTATCCACCTGGTGGGATACGAGCCCAATT 180
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Qy 181 CGAAGAAAGTCAGTCATGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Qy 241 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 300
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Db 364 TGTGATGCTGGAGGTGGAGTGGTATTATATAGGCTCAGCCAAAGACATGCTGATAATC 423
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RESULT 4

E11466
LOCUS CDNA encoding tyrosinase. 2384 bp RNA linear PAT 29-SEP-1997
DEFINITION E11466
ACCESSION E11466
VERSION E11466.1 GI:22025102
KEYWORDS JP 1996140699-A/1.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2384)
Shibata,T., Suzuki,S., Takimoto,H. and Masui,S.
MEASUREMENT OF TYROSINASE MESSENGER RNA AMOUNT
Patent: JP 1996140699-A 1 04-JUN-1996;
POLA CHEM IND INC
OS Homo sapiens (human)
PN JP 1996140699-A/1
PD 04-JUN-1996
PF 22-NOV-1994 JP 1994288041
PI SHIBATA TAKASHI, SUZUKI SATOSHI, TAKIMOTO HIROYUKI, PI MASUI
SHIGEKI
PC C12Q1/68,C12N15/09;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FH source 1..2384
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FT /tissue_type='Skin'
FT /cell_type='melanocyte'
FT 5'UTR 1..502
FT CDS 503..2092
FT /product='tyrosinase'
FT 3'UTR 2093..2384.
FT Location/Qualifiers
1..2384
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/db_xref='taxon:9606'

FEATURES

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BASE COUNT 652 a 533 c 520 g 679 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 244 GGTCAATAGAGTTTTCACCTTACATAGGCCTATCCACTGGTGGGATAGACCAATT 303
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DB 304 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGCTAAAG 363
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FEATURES

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Best Local Similarity 100.0%; Pred. No. 7.1e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 5

I49609
LOCUS CDNA encoding tyrosinase. 2384 bp DNA linear PAT 07-OCT-1997
DEFINITION I49609
ACCESSION I49609
VERSION I49609.1 GI:2471829
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2384)
AUTHORS Li,L. and Lishko,V.K.
TITLE Method for delivering melanin to hair follicles
JOURNAL Patent: US 5641508-A 1 24-JUN-1997;
FEATURES Location/Qualifiers
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/organism='Homo sapiens'
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ACCESSION

I49609
VERSION I49609.1 GI:2471829
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2384)
AUTHORS Li,L. and Lishko,V.K.
TITLE Method for delivering melanin to hair follicles
JOURNAL Patent: US 5641508-A 1 24-JUN-1997;
FEATURES Location/Qualifiers
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Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 184 AGGCATTATTATTACTAACTTATTTGTTAATATTTCTAACCATAGAAATTAACATTAAT 243
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QY 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGCTAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGCTAAAG 363
QY 241 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGGTTCTCAGCCAAAGCATGTGATATC 300
DB 364 TGTTTGATGCTGGAGGTGGGAGTGGTATTATATAGGTTCTCAGCCAAAGCATGTGATATC 423

RESULT 6

HUMTYRA HUMTYRA 2384 bp mRNA linear PRI 02-DEC-1996
LOCUS Human tyrosinase (TYR) mRNA, complete cds.
DEFINITION M27160
ACCESSION M27160
VERSION M27160.1 GI:1698397
KEYWORDS tyrosinase.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 601 to 2384)
Shibahara,S., Tomita,Y., Tagami,H., Muller,R.M. and Cohen,T.
TITLE Molecular basis for the heterogeneity of human tyrosinase
JOURNAL Tohoku J. Exp. Med. 156 (4), 403-414 (1988)
MEDLINE 89222868
PUBMED 2854305
REFERENCE 2 (bases 1 to 600)
Takeda,A., Tomita,Y., Okinaga,S., Tagami,H. and Shibahara,S.
AUTHORS Functional analysis of the cDNA encoding human tyrosinase precursor
TITLE Biochem. Biophys. Res. Commun. 162 (3), 984-990 (1989)
JOURNAL 89351001
MEDLINE 2504160
PUBMED
COMMENT On Dec 2, 1996 this sequence version replaced gi:340036.
Draft entry and computer-readable copy of sequence [1] kindly
provided by S.Shibahara, 15-AUG-1989.
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552 a 533 c 520 g 679 t

BASE COUNT 652 a 533 c 520 g 679 t
ORIGIN

Query Match 100.0%; Score 300; DB 9; Length 2384;
Best Local Similarity 100.0%; Pred. No. 7,le-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTTGCAAGTCAATCATCATTTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 60
Db 124 TCATTTGCAAGTCAATCATCATTTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 183
QY 61 AGGCATTATTACTAACTTATCTTAACTTAACTAACTAACTAACTAACTAACT 120
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Db 364 TGTTTGATGCTGGAGTGGAGTGGTATTATATAGGCTCTCAGCCAAAGACATGTGATAATC 423

RESULT 7
HSTYROIE 3586 bp DNA linear PRI 20-NOV-1998
LOCUS Human tyrosinase gene, exon 1 and 5' flanking region (EC
DEFINITION 1.14.18.1).
ACCESSION X16073
VERSION 1
KEYWORDS monophenol monooxygenase; tyrosinase.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Euteleostomi;
REFERENCE 1 (bases 1 to 3586)
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Kikuchi, H.
Direct Submission
Submitted (03-AUG-1989) Kikuchi H., The Res. Inst. for TB and
Cancer, Tohoku University, 1-4 Seiryomachi, Sendai 980, JAPAN
REFERENCE 2 (bases 1 to 3586)
AUTHORS Kikuchi, H., Miura, H., Yamamoto, H., Takeuchi, T., Del. T. and
Watanabe, M.
TITLE Characteristic sequences in the upstream region of the human
tyrosinase gene
JOURNAL Biochim. Biophys. Acta 1009 (3), 283-286 (1989)
MEDLINE 90089403
PubMed 2480811
COMMENT Data kindly reviewed (01-FEB-1990) by Kikuchi H.
FEATURES
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Location/Qualifiers
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133..175
repeat_region
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281..288
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464..471
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/notes="CAMP responsive element"
572..582
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661..668
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753..762
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781..788
CAAT_signal
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876..881
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misc_feature
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908..1805
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987..1805
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/translation="MLAVLYCLWSFOTSGAHFPRACVSSKNLMEKCCPPWSGDRS
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BASE COUNT 1126 a 636 c 761 g 1063 t
ORIGIN

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QY 1 TCATTTGCAAGTCAATCATCATTTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 60
Db 608 TCATTTGCAAGTCAATCATCATTTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC 667
QY 61 AGGCATTATTACTAACTTATCTTAACTTAACTAACTAACTAACTAACTAACT 120
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Db 668 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCAATAAGAATTAAACTATTAAAT 727
Qy 121 GGTGAATAGAGTTTTCACATTAACATAGGCTTATCCACACTGGTGGGATACGAGCCCAATT 180
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Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Db 788 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 847
Qy 241 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGACATGTCATATC 300
Db 848 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGACATGTCATATC 907

RESULT 8
LOCUS AP000720 147357 bp DNA linear PRI 23-MAY-2001
DEFINITION Homo sapiens genomic DNA, chromosome 11q clone:RP11-796A5, complete
sequences.
ACCESSION AP000720
VERSION AP000720.4 GI:14189775
KEYWORDS HTG.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (sites)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Homo sapiens genomic DNA
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 147357)
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P.,
Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1999) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.ygc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT On May 22, 2001 this sequence version replaced gi:9927289.
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/chromosome="11"
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ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 3.5e-58;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCATTTGCAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGCTTAGGTC 60
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Qy 61 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCAATAAGAATTAAACTATTAAAT 120
Db 1776 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCAATAAGAATTAAACTATTAAAT 1835

Qy 121 GGTGAATAGAGTTTTCACATTAACATAGGCTTATCCACACTGGTGGGATACGAGCCCAATT 180
Db 1836 GGTGAATAGAGTTTTCACATTAACATAGGCTTATCCACACTGGTGGGATACGAGCCCAATT 1895

Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
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Db 1956 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGCATGTCTAATC 2015

RESULT 9
LOCUS PAPATYR1 1563 bp DNA linear PRI 29-OCT-2000
DEFINITION Pan paniscus tyrosinase gene, exon 1.
ACCESSION AF183588
VERSION AF183588.1 GI:11036743
KEYWORDS 1 of 5
SEGMENT SOURCE
ORGANISM Pan paniscus.
Pan paniscus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE 1 (bases 1 to 1563)
AUTHORS Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.
TITLE Molecular evolution of tyrosinase gene in primates
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular
Evolution, Kunming Institute of Zoology, the Chinese Academy of
Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 550223, P.R. China
FEATURES
source
1. 1563
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BASE COUNT 449 a 332 c 336 g 446 t
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Matches 296; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 309 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCAATAAGAATTAAACTATTAAAT 368

Qy 121 GGTGAATAGAGTTTTCACATTAACATAGGCTTATCCACACTGGTGGGATACGAGCCCAATT 180
Db 369 GGTGAATAGAGTTTTCACATTAACATAGGCTTATCCACACTGGTGGGATACGAGCCCAATT 428

Qy 181 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Db 429 CGAAGAAAAGTCAGTCATGCTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 488

Qy 241 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGACATGTCATATC 300
Db 489 TGTTCATGCTGGAGGTGGAGTGGTATTATATAGGTCCTCAGCCAAAGACATGTCATATC 548

RESULT 10
LOCUS PTTYR1 1563 bp DNA linear PRI 26-OCT-2000
DEFINITION Pan troglodytes tyrosinase gene, exon 1.
ACCESSION AF183588
VERSION AF183588.1 GI:11023097
KEYWORDS 1 of 5
SEGMENT SOURCE
ORGANISM Pan troglodytes.
Pan troglodytes.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.
REFERENCE 1 (bases 1 to 1563)

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AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Molecular evolution of tyrosinase gene in primates
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1563)
AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular Evolution, Kunming Institute of Zoology, the Chinese Academy of Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R. China

FEATURES
source Location/Qualifiers
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/db_xref="taxon:9598"
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/number=1
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ORIGIN

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Best Local Similarity 98.3%; Pred. No. 4.8e-56;
Matches 295; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 61 AGCCATTATTACTAACTTTATGTTAATATCTCAACCAATAAGAAATTAACATAAT 120
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QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGCGCTATCCCACTGGTGGATACGACCAAT 180
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Db 369 GTGAATAGAGTTTTCACCTTAAACATAGCGCTATCCCACTGGTGGATACGACCAAT 428
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QY 181 CGAAGAAAAGTCAGTCATGCTTTTCAGAGATGAAAGCTTAAGATAAGACTAAAAG 240
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Db 429 CCAAGAAAAGTCAGTCATGCTTTTCAGAGATGAAAGCTTAAGATAAGACTAAAAG 488
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QY 241 TGTTCATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
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Db 489 TGTTCATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 548
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RESULT 11
HSU03039
LOCUS HSU03039 2311 bp DNA linear PRI 06-AUG-1994
DEFINITION Human tyrosinase gene, promoter region.
ACCESSION U03039
VERSION U03039.1 GI:414980
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2311)
Ponnazhagan, S., Hou, L. and Kwon, B.S.
STRUCTURAL organization of the human tyrosinase gene and sequence analysis and characterization of its promoter region
J. Invest. Dermatol. 102 (5), 744-748 (1994)
94231032
PUBMED 8176257
REFERENCE 2 (bases 1 to 2311)
Kwon, B.S.
AUTHORS Direct Submission
TITLE Submitted (29-OCT-1993) Kwon B.S., Indiana University School of Medicine, Microbiology and Immunology, 635 Barnhill Dr, Indianapolis, IN 46202, USA
JOURNAL Location/Qualifiers
1..2311 /organism="Homo sapiens"
/db_xref="taxon:9606"
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BASE COUNT 796 a 396 c 493 g 626 t
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Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTTCGAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 60
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Db 1929 TCATTTCGAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 1988
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QY 61 AGCCATTATTACTAACTTTATGTTAATATCTCAACCAATAAGAAATTAACATAAT 120
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Db 1989 AGCCATTATTACTAACTTTATGTTAATATCTCAACCAATAAGAAATTAACATAAT 2048
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Db 2049 GGTGAATAGAGTTTTCACCTTAAACATAGCGCTATCCCACTGGTGGATACGACCAAT 2108
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QY 181 CGAAG-AAAAGTCAGTCATGCTTTTCAGAGATGAAAGCTTAAGATAAGACTAAA 239
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Db 2109 CGAAGAAAAGTCAGTCATGCTTTTCAGAGATGAAAGCTTAAGATAAGACTAAA 2168
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QY 240 GTGTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAAT 299
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Db 2169 GTGTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAAT 2228
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QY 300 c 300
Db 2229 c 2229

RESULT 12
I70158
LOCUS I70158 2397 bp DNA linear PAT 02-APR-1998
DEFINITION Sequence 11 from patent US 5679511.
ACCESSION I70158
VERSION I70158.1 GI:3006293
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2397)
AUTHORS Kwon, B.S.
TITLE CDNA clones for a regulatory protein in the melanin-production pathway
JOURNAL Patent: US 5679511-A 11 21-OCT-1997;
FEATURES Location/Qualifiers
source 1..2397 /organism="unknown"
BASE COUNT 808 a 427 c 507 g 655 t
ORIGIN

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Best Local Similarity 99.7%; Pred. No. 2.1e-55;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTTCGAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 60
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Db 1926 TCATTTCGAAGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 1985
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QY 61 AGCCATTATTACTAACTTTATGTTAATATCTCAACCAATAAGAAATTAACATAAT 120
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Db 1986 AGCCATTATTACTAACTTTATGTTAATATCTCAACCAATAAGAAATTAACATAAT 2045
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QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGCGCTATCCCACTGGTGGATACGACCAAT 180
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Db 2046 GGTGAATAGAGTTTTCACCTTAAACATAGCGCTATCCCACTGGTGGATACGACCAAT 2105
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LOCUS	COPOYR1	1558 bp	DNA	linear	PRI 29-OCT-2000
DEFINITION	Colobus polykomos tyrosinase gene, exon 1.				
ACCESSION	AF183593				
VERSION	AF183593.1	GI:11036702			
KEYWORDS					
SEGMENT					
SOURCE	1 of 5				
ORGANISM	Colobus polykomos.				
	Colobus polykomos				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;				
	Colobinae; Colobus.				
REFERENCE	1 (bases 1 to 1558)				
AUTHORS	Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.				
TITLE	Molecular evolution of tyrosinase gene in primates				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1558)				
AUTHORS	Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.				
TITLE	Direct Submission				
JOURNAL	Submitted (09-SEP-1999) Laboratory of Cellular and Molecular				
	Evolution, Kunming Institute of Zoology, The Chinese Academy of				
	Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunan 650223, P.R.China				
FEATURES	Location/Qualifiers				
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Qy	61 AGGCATTATTATTACTAACCTATTGTTTAAATATTCTTAACCATAGAATTAACACTAATTAAT 120				
Db	303 AGGCATTATTATTATTATCTATTGTTTAAATATTCTTAACCATAGAATTAACACTAATTAAT 362				
Qy	121 GGTGAATAGAGTTTTTTCACCTTAACATAGGCTATCCACATGGTGGGATAGAGCAAT 180				
Db	363 GGTGAATAGAGTTTTTTCACCTTAACATAGAGCTATCCACATGGTGGGATAGAGCAAT 422				
Qy	181 CGAAGAAAAGCTCAGTCATGTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACTATAAAG 240				
Db	423 CCAAGAAAAGCTCAGTCATGTGCTTTTCAGAGGATAAAGCTTAAGATAAAGACTATAAAG 482				
Qy	241 TGTTTGATGCTGGAGGTGGGAGTGATATATATAGGTCACGCCAAGACATGTGTATATC 300				
Db	483 TGTTTGATGCTGGAGGTGGGAGTGATATATATAGGTCACGCCAAGACATGTGTATATC 542				
RESULT 15					
MATYR1					
LOCUS	MATYR1	1558 bp	DNA	linear	PRI 01-NOV-2000
DEFINITION	Macaca arctoides tyrosinase gene, exon 1.				
ACCESSION	AF183614				
VERSION	AF183614.1	GI:1105814			
KEYWORDS					
SEGMENT					
SOURCE	1 of 5				
ORGANISM	Macaca arctoides.				
	Macaca arctoides				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;				
	Cercopitheciinae; Macaca.				
REFERENCE	1 (bases 1 to 1558)				
AUTHORS	Ding,B., Ryder,O.A., Shi,P. and Zhang,Y.-P.				
TITLE	Molecular evolution of tyrosinase gene in primates				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 1558)				

AUTHORS Ding, B., Ryder, O.A., Shi, P. and Zhang, Y.-P.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1999) Laboratory of Cellular and Molecular
Evolution, Kunming Institute of Zoology, The Chinese Academy of
Sciences, 32 Jiao Chang Dong Lu, Kunming, Yunnan 650223, P.R. China

FEATURES Location/Qualifiers

Source
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/organism="Macaca arctoides"
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BASE COUNT 445 a 329 c 343 g 441 t
ORIGIN

Query Match 95.7%; Score 287.2; DB 9; Length 1558;
Best Local Similarity 97.3%; Pred. No. 5.8e-55;
Matches 292; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
QY 1 TCATTTGCAAGTCAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 60
Db 243 TCATCTGCAAGTTCAATCATCATCTAGTTTGTAGTCTATTAACTGGGTTTGGTTAGGTC 302
QY 61 AGGCATTATTATTACTAACTTATCTTAATATTCTAACCATTAAGAAATTAACCTATTAAT 120
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Db 363 GGTGAATAGAGTTTTCACCTTTAACATAGACCTATCCCACTGGTGGGATATGAGCCAATT 422
QY 181 CGAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAGCTTAAGATAAGACTAAAAG 240
Db 423 CCAAGAAAAGTCAGTCATGTGCTTTTCAGAGGATGAAGCTTAAGATAAGACTAAAAG 482
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OM nucleic - nucleic search, using sw model

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2588.504 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

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Post-processing: Minimum Match 0%

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SUMMARIES

Result NO.	Score	Query Match	Length	ID	Description
1	300	100.0	300	22 AAC86171	Tyr300. Homo sapi
2	300	100.0	300	23 AAS14779	Melanoma-specific
3	300	100.0	2384	15 AAQ72871	Human tyrosinase g
4	300	100.0	2384	17 AAT33316	Tyrosinase mRNA.
5	300	100.0	3586	15 AAQ56643	Human tyrosinase g
6	289	96.3	2397	18 AAT95736	Human tyrosinase g
7	235	78.3	3586	24 AAS63366	Chemically pretrea
8	219	73.0	546	22 AAH43616	Tyrosinase-TRE. H
9	219	73.0	546	23 AAF87236	Tyrosinase-TRE fus

c 10	202.4	67.5	3586	24	AAS63367	Chemically pretrea
c 11	67	22.3	4752	15	AAQ58032	Tyrosinase promote
c 12	42.4	14.1	1212	21	AAA70218	Plasmodium falcipa
c 13	40.8	13.6	7195	22	AAS45324	Chemically pretrea
c 14	40.8	13.6	7195	24	ABK28165	DNA transcription
c 15	40	13.3	2041	22	AAS60958	Human cancer agent
c 16	38.8	12.9	3582	21	AAA70241	Plasmodium falcipa
c 17	38.2	12.7	9021	22	AAS46326	Tyrosinase suppressor
c 18	37.8	12.6	15767	24	ABL33207	Human immune syste
c 19	37.8	12.6	15767	24	ABL34553	Human metastasis a
c 20	37.6	12.5	382	21	ABN81050	Shrimp polynucleot
c 21	37.2	12.4	2270	23	ABL24848	Drosophila melanog
c 22	37.2	12.4	1143	23	ABL12834	Drosophila melanog
c 23	37	12.3	5454	21	AAA70236	Plasmodium falcipa
c 24	36.6	12.2	357	21	AZ94801	Soybean microsatel
c 25	36.6	12.2	580	21	ABN81132	Shrimp polynucleot
c 26	36.6	12.2	2924	22	AAH55011	S. epidermidis gen
c 27	36.6	12.2	3037	22	AAH54537	S. epidermidis gen
c 28	36.6	12.2	3241	22	AAH54912	S. epidermidis gen
c 29	36.4	12.1	944	23	ABL13085	Drosophila melanog
c 30	36.4	12.1	1835	23	ABL20020	Drosophila melanog
c 31	36.4	12.1	1835	23	ABL20898	Drosophila melanog
c 32	36.4	12.1	2948	23	ABL13084	Drosophila melanog
c 33	36.4	12.1	6642	23	ABL05270	Drosophila melanog
c 34	36.4	12.1	10810	23	ABL13100	Drosophila melanog
c 35	36.4	12.1	10992	23	ABL05242	Drosophila melanog
c 36	36.4	12.1	15649	22	AAS45396	Chemically pretrea
c 37	36.4	12.1	15649	24	ABK28241	LNA transcription
c 38	36.2	12.1	925	21	ABN81142	Shrimp polynucleot
c 39	36.2	12.1	6033	21	AAA70152	Plasmodium falcipa
c 40	36.2	12.1	8654	23	ABL04334	Drosophila melanog
c 41	36.2	12.1	12943	23	ABL20980	Drosophila melanog
c 42	36	12.0	373	21	ABN81130	Shrimp polynucleot
c 43	36	12.0	1452	21	AAA70123	Plasmodium falcipa
c 44	36	12.0	19576	24	ABL70576	Chemically treated
c 45	36	12.0	19576	24	AAS61259	Human gene regulat

ALIGNMENTS

RESULT 1

AAC86171
ID AAC86171 standard; cDNA; 300 BP.

XX AAC86171;

XX 19-SEP-2001 (first entry)

XX Tyr300.

XX Melanoma-specific promoter; human; tyrosinase gene; Tyr300; M box;

XX activator; transgene expression; gene therapy; tumour; melanoma; ss.

XX Homo sapiens.

XX Key Location/Qualifiers

FT misc_signal 194..204

FT /*tag= a

FT /label= "M box"

XX WO200138488-A2.

XX 31-MAY-2001.

XX 22-NOV-2000; 2000WO-US32203.

XX 23-NOV-1999; 99US-0167085.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.

XX Vile R, Gough M;

XX


```

XX cyclosporin A; macromolecule; polymer; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 503..2092
XX FT /*tag= a
XX FT /product= human tyrosinase
XX
XX WO9422468-A.
XX
XX 13-OCT-1994.
XX
XX 01-APR-1994; 94WO-US03634.
XX
XX 02-APR-1993; 93US-0041553.
XX 13-JAN-1994; 94US-0181471.
XX
XX (ANTI-) ANTICANCER INC.
XX
XX Li L, Lishko VK;
XX
XX WPI; 1994-332816/11.
XX P-PSDB; AAR63623.
XX
XX Liposomes for delivering protein, nucleic acid etc. to hair
XX follicles - e.g. to restore hair colour, prevent hair loss during
XX chemotherapy, stimulate hair growth etc.
XX
XX Claim 6; Page 67-70; 10pp; English.
XX
XX The nucleotide sequence of a human tyrosinase gene. This is an example
XX of a compound which can be delivered to hair follicles via a novel
XX liposome composition. The liposomes are comprised of a lipophilic or
XX lipophobic compound which will selectively target the hair follicle
XX (via the stratum corneum) without damaging or unwanted effects on cells
XX outside the follicle. Compounds e.g. tyrosinase (or the DNA encoding
XX it), melanin or hair dyes, can be delivered to the hair follicle to
XX restore hair colour or condition. Other compounds targeted at hair
XX follicles can include: p-glycoprotein (AAQ72872) (for treatment of
XX chemotherapy-induced alopecia); human transforming growth factor alpha
XX (AAQ2873) (for reversal of wavy hair); hair growth stimulants (e.g.
XX cyclosporin A or aramase) or antisense sequences. The methods allows
XX compounds (e.g. macromolecules or polymers), which would not normally
XX reach the hair follicles, to be delivered to these target areas.
XX
XX Sequence 2384 BP; 652 A; 534 C; 519 G; 679 T; 0 other;

Query Match 100.0%; Score 300; DB 15; Length 2384;
Best Local Similarity 100.0%; Pred. No. 4.9e-68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTTCGAAGTCAATCATCATCTAGTTTGTAGTCTATTAACTGGTTGCTTAGGTC 60
Db 124 TCATTTCGAAGTCAATCATCATCTAGTTTGTAGTCTATTAACTGGTTGCTTAGGTC 183
QY 61 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAACTTAACTATTAAT 120
Db 184 AGGCATTATTATTACTAACCTTATTGTTAATATTCTAACCATAGAACTTAACTATTAAT 243
QY 121 GGTGAATAGAGTTTTTCACCTTTAACATPAGCCCTATCCCACTGGTGGGATACGAGCCAATT 180
Db 244 GGTGAATAGAGTTTTTCACCTTTAACATPAGCCCTATCCCACTGGTGGGATACGAGCCAATT 303
QY 181 CGAAGAAAGTCAAGTCATGCTGCTTTTCAGAGGATGAACTTAACTAAGACTAAAG 240
Db 304 CGAAGAAAGTCAAGTCATGCTGCTTTTCAGAGGATGAACTTAACTAAGACTAAAG 363
QY 241 TGTTTGATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCAGACATGTGATAATC 300
Db 364 TGTTTGATGCTGGAGTGGAGTGGTATTATATAGGTCTCAGCCAGACATGTGATAATC 423

RESULT 4
AAT33316
ID AAT33316 standard; CDNA to mRNA; 2384 BP.
XX
XX AC AAT33316;
XX
XX DT 18-OCT-1996 (first entry)
XX
XX DE Tyrosinase mRNA.
XX
XX KW Human; tyrosinase; detection; primer; reverse transcription; amplify;
XX KW transcription region; detection; ds.
XX
XX OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 503..2092
XX FT /*tag= a
XX FT /product= Tyrosinase
XX FT 790..810
XX FT /*tag= b
XX FT /note= "Binds primer given in AAT33323"
XX FT 881..901
XX FT /*tag= c
XX FT /note= "Binds primer given in AAT33321"
XX FT 1297..1317
XX FT /*tag= d
XX FT /note= "Binds primer given in AAT33317"
XX FT 1327..1347
XX FT /*tag= e
XX FT /note= "Binds primer given in AAT33319"
XX FT complement (1521..1541)
XX FT /*tag= f
XX FT /note= "Binds primer given in AAT33318"
XX FT complement (1600..1620)
XX FT /*tag= g
XX FT /note= "Binds primer given in AAT33332"
XX FT complement (1650..1670)
XX FT /*tag= h
XX FT /note= "Binds primer given in AAT33320"
XX FT complement (1673..1693)
XX FT /*tag= i
XX FT /note= "Binds primer given in AAT33324"
XX
XX JP08140699-A.
XX
XX 04-JUN-1996.
XX
XX 22-NOV-1994; 94JP-0288041.
XX
XX 22-NOV-1994; 94JP-0288041.
XX (POKK ) POLA CHEM IND INC.
XX
XX WPI; 1996-316329/32.
XX P-PSDB; AAW00184.
XX
XX Detection of tyrosinase mRNA - by amplification of tyrosinase mRNA
XX allows accurate detection of trace amounts of RNA
XX
XX Disclosure; Page 7-9; 10pp; Japanese.
XX
XX This sequence encodes human tyrosinase. This sequence was detected
XX by the method of the invention using the primers given in AAT33317-24.
XX The method comprises synthesising tyrosinase cDNA from a sample by
XX reverse transcription and then amplifying the cDNA using primers
XX specific for, or complementary to, sequences within the transcription
XX region of the tyrosinase gene. Amplification using these primers
XX produces a competitive cDNA which can also be amplified. This method
XX can be used to specifically detect trace amounts of human tyrosinase
XX mRNA.
XX
XX Sequence 2384 BP; 652 A; 533 C; 520 G; 679 T; 0 other;
```

Query Match 100.0%; Score 300; DB 17; Length 2384;
Best Local Similarity 100.0%; Pred. No. 4.9e-69; Indels 0; Gaps 0;
Matches 300; Conservative 0; Mismatches 0;

QY 1 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTTCTTAGGTC 60
DB 124 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTTCTTAGGTC 183

QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTTAACTTAACCATTAAGAAATAACTATTAA 120
DB 184 AGGCATTATTATTACTAACCTTATTGTTAAATTTTAACTTAACCATTAAGAAATAACTATTAA 243

QY 121 GGTGAATAGAGTTTTCACCTTTAAACATAGGCTATCCACCTGGTGGGATACGAGCCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTTAAACATAGGCTATCCACCTGGTGGGATACGAGCCAATT 303

QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 363

QY 241 TGTTCATGCTGGAGTGGAGTGTATATATAGTCTCAGCCCAAGACATGTGATAATC 300
DB 364 TGTTCATGCTGGAGTGGAGTGTATATATAGTCTCAGCCCAAGACATGTGATAATC 423

RESULT 5
AAQ56643
ID AAQ56643 standard; DNA; 3586 BP.
XX AC AAQ56643;
XX AC AAQ56643;
DT 16-SEP-1994 (first entry)
XX DE Human tyrosinase gene.
XX DE Tyrosinase; albino; albinism; detection; diagnosis;
KW Tyrosinase; albino; albinism; detection; diagnosis;
KW treatment; prevention; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT CDS 987..1805
FT /*tag= a
FT /product= Tyrosinase.
FT /note= "CDS excludes termination codon."
XX PN JP06000100-A.
XX PD 11-JAN-1994.
XX PF 18-JUN-1992; 92JP-0185885.
XX PR 18-JUN-1992; 92JP-0185885.
XX PA (DAI) DAICEL CHEM IND LTD.
XX DR WPI; 1994-077141/10.
XX P-PSDB; AAR48368.
XX A DNA sequence which hybridises to the human tyrosinase gene -
PT used for the detection, diagnosis, prevention and treatment of
PT human albinism
XX Disclosure: Page 5-7; 8pp; Japanese.
XX A DNA sequence having at least 12 successive bases and which
CC hybridises upstream and/or downstream of the 310th base from the
CC transcription start site of the human tyrosinase gene can be
CC used for the detection, diagnosis, prevention and treatment of human
CC albinism.
XX Sequence 3586 BP; 1127 A; 636 C; 760 G; 1063 T; 0 other;

Query Match 100.0%; Score 300; DB 15; Length 3586;
Best Local Similarity 100.0%; Pred. No. 5.3e-68; Indels 0; Gaps 0;
Matches 300; Conservative 0; Mismatches 0;

QY 1 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTTCTTAGGTC 60
DB 608 TCATTGCAAGTCAAAATCATCATTTGTTAGTCTATTAACTGGGTTTCTTAGGTC 667

QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTTAACTTAACCATTAAGAAATAACTATTAA 120
DB 668 AGGCATTATTATTACTAACCTTATTGTTAAATTTTAACTTAACCATTAAGAAATAACTATTAA 727

QY 121 GGTGAATAGAGTTTTCACCTTTAAACATAGGCTATCCACCTGGTGGGATACGAGCCAATT 180
DB 728 GGTGAATAGAGTTTTCACCTTTAAACATAGGCTATCCACCTGGTGGGATACGAGCCAATT 787

QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 240
DB 788 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 847

QY 241 TGTTCATGCTGGAGTGGAGTGTATATATAGTCTCAGCCCAAGACATGTGATAATC 300
DB 848 TGTTCATGCTGGAGTGGAGTGTATATATAGTCTCAGCCCAAGACATGTGATAATC 907

RESULT 6
AAT95736
ID AAT95736 standard; DNA; 2397 BP.
XX AC AAT95736;
XX AC AAT95736;
DT 13-MAR-1998 (first entry)
XX DE Human tyrosinase gene promoter.
XX DE Pmel17; lambda mel 17-1; ATCC 40264; melanisation; human; melanin;
KW melanocyte; biosynthesis; determination; Northern blot analysis;
KW probe; tyrosinase; gene promoter; ds.
XX OS Homo sapiens.
XX PN US5679511-A.
XX PD 21-OCT-1997.
XX PF 01-JUN-1992; 92US-0891942.
XX PR 01-JUN-1992; 92US-0891942.
XX PR 06-OCT-1986; 86US-0915753.
XX PR 07-JUN-1989; 89US-0362847.
XX PA (GUTH-) GUTHRIE FOUND MEDICAL RES INC DONALD.
XX PA (INDV) UNIV INDIANA FOUND.
XX PI Kwon BS;
XX WPI; 1997-525715/48.
XX Lambda mel 17-1 cDNA and Pmel17 protein - useful as melanin
PT biosynthesis probe
XX Disclosure; Columns 73-74; 67pp; English.
XX The present sequence is disclosed in the specification, which
CC describes the isolation of Pmel17, a protein encoded by cDNA
CC isolated from lambda mel 17-1 (ATCC 40264). The degree of
CC melanisation in a human melanocyte can be determined by subjecting
CC human melanocyte RNA to a Northern blot analysis, using the cDNA
CC as a probe.
XX Sequence 2397 BP; 808 A; 427 C; 507 G; 655 T; 0 other;

```
Query Match 96.3%; Score 289; DB 18; Length 2397;
Best Local Similarity 99.7%; Pred. No. 3.4e-65;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTTCGACAGGTCACATCATCATCTAGTTTGTAGTCTATTACTGGTTTGCTTAGGTC 60
DB 1926 TCATTTCGACAGGTCACATCATCTAGTTTGTAGTCTATTACTGGTTTGCTTAGGTC 1985

QY 61 AGCCATTATTACTAACTTATCTGTTAATATCTTAACCATAGAACTTAACTATTAAAT 120
DB 1986 AGCCATTATTACTAACTTATCTGTTAATATCTTAACCATAGAACTTAACTATTAAAT 2045

QY 121 GGTGAATAGAGTTTTTCACTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAT 180
DB 2046 GGTGAATAGAGTTTTTCACTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAT 2105

QY 181 CGAAG-AAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAGATATAAGACATAAA 239
DB 2106 CGAAGAAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAGATATAAGACATAAA 2165

QY 240 GTCTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCTCAGCCAGACATCTGATAAT 299
DB 2166 GTCTTTGATGCTGGAGTGGAGTGGTATTATATAGTCTCTCAGCCAGACATCTGATAAT 2225

QY 300 C 300
DB 2226 C 2226

RESULT 7
AAS63366
ID AAS63366 standard; DNA; 3586 BP.
AC AAS63366;
XX
DT 29-JAN-2002 (first entry)
DE Chemically pretreated metabolism associated gene #61.
KW Human; cytostatic; anti-tumour; metabolism; metabolic disease; liver;
KW solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
KW single nucleotide polymorphism detection; SNP; stool; urine; lung;
KW cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
KW DUSP2; EPHX2; QDPR; SGSH; SHMT2; SLC7A4; TYMS; ds.
XX
OS Homo sapiens.
XX
XX WO200176451-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-EP04016.
XX
XX 06-APR-2000; 2000DE-1019058.
XX
XX 07-APR-2000; 2000DE-1019173.
XX
XX 30-JUN-2000; 2000DE-1032529.
XX
XX 01-SEP-2000; 2000DE-1043826.
XX
XX (EPIC-) EPICENOMICS AG.
XX
XX Olek A, Piepenbrock C, Berlin K;
XX
XX WPI; 2002-010834/01.
XX
XX New nucleic acid, useful for diagnosis and therapy of metabolic
XX disease, solid tumour and cancers, comprises segment of chemically
XX modified genomic sequences of genes associated with metabolism -
XX
XX Claim 1; Page 140-141; 143pp; English.
XX
XX The invention relates to a nucleic acid (I) comprising a sequence at
XX least 18 bases of a segment of the chemically pretreated DNA of genes
XX associated with metabolism such as DUSP2 (NM_004418), EPHX2 (NM_001979),
XX
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```
CC QDPR (NM_000320), SGSH (NM_000199), SHMT2 (NM_005412), SLC7A2
CC (NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all
CC undefined). (I) are useful for diagnosis and therapy of metabolic
CC disease, solid tumours and cancers, as primer oligonucleotides for the
CC amplification of DNA sequences, for detecting the cytosine methylation
CC state and/or single nucleotide polymorphisms (SNPs) in a chemically
CC treated DNA of genes associated with metabolism. An array of (I) is
CC useful for ascertaining genetic and/or epigenetic parameters for the
CC diagnosis and/or therapy of existing diseases or the predisposition to
CC specific diseases by analysing cytosine methylations. The method involves
CC chemically treating genomic DNA sample by a solution of bisulphite,
CC hydrogen sulphite or disulphite such that cytosine bases which are
CC unmethylated at the 5th-position are converted to uracil or another base
CC which is dissimilar to cytosine in terms of hybridisation behaviour and
CC amplifying fragments of the chemically pretreated genomic DNA. The
CC genomic DNA is from cells or cellular components which contain DNA,
CC sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum,
CC stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as
CC tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast
CC or liver, histologic object slides and their combinations. Genetic
CC parameters are mutations, in particular insertions, deletions, point
CC mutations, inversions and polymorphisms of genes associated with
CC metabolism and sequences further required for their regulation.
CC Epigenetic parameters are in particular cytosine methylations and
CC further chemical modifications of DNA bases of genes associated with
CC metabolism. Further epigenetic parameters include for e.g. the
CC acetylation of histones which correlates with DNA methylation.
CC AAS63306-AAS63373 represent chemically pretreated metabolism associated
CC genes, and related primers of the invention.
XX
XX Sequence 3586 BP; 1126 A; 22 C; 761 G; 1677 T; 0 other;
SQ
Query Match 78.3%; Score 235; DB 24; Length 3586;
Best Local Similarity 86.6%; Pred. No. 3.2e-51;
Matches 259; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 TCATTTCGACAGGTCACATCATCTAGTTTGTAGTCTATTACTGGTTTGCTTAGGTC 60
DB 608 TTATTTCGACAGGTCACATCATCTAGTTTGTAGTCTATTACTGGTTTGCTTAGGTC 667

QY 61 AGCCATTATTACTAACTTATCTGTTAATATCTTAACCATAGAACTTAACTATTAAAT 120
DB 668 AGCCATTATTACTAACTTATCTGTTAATATCTTAACCATAGAACTTAACTATTAAAT 727

QY 121 GGTGAATAGAGTTTTTCACTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAT 180
DB 728 GGTGAATAGAGTTTTTCACTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAT 787

QY 181 CGAAGAAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAGATATAAGACATAAAAG 240
DB 788 CGAAGAAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAGATATAAGACATAAAAG 847

QY 241 TGTTCGATGCTGGAGTGGAGTGGTATTATATAGTCTCTCAGCCAGACATGTGATAAT 299
DB 848 TGTTCGATGCTGGAGTGGAGTGGTATTATATAGTCTCTCAGCCAGACATGTGATAAT 906

RESULT 8
AAH43616
ID AAH43616 standard; cDNA; 546 BP.
XX
XX AC AAH43616;
XX
XX 07-JAN-2002 (first entry)
XX
XX Tyrosinase-TRE.
XX
XX Adenovirus; ADP; replication-competent; adenoviral vector; TRE; PCR;
XX transcriptional regulatory element; mutation; deletion; IRFS; primer;
XX promoter; internal ribosome entry site; cytotoxic; cancer; bladder;
XX amplifi; polymerase chain reaction; alpha-fetoprotein; AFP; EMCV;
XX encephalomyocarditis virus; vascular endothelial growth factor; VEGF;
XX immunoglobulin heavy-chain binding protein; BiP; uroplakin II; PDGF;
```

KW platelet derived growth factor; ss.
 XX Homo sapiens.
 OS WO200173093-A2.
 PN 04-OCT-2001.
 PD 21-MAR-2001; 2001WO-US09036.
 PF 24-MAR-2000; 2000US-192156P.
 PR (CALY-) CALYDON INC.
 PA Yu D, Li Y, Henderson DR;
 PI WPI; 2001-639234/73.
 DR Replication-competent adenoviral vector, useful e.g. for killing cancer
 PT cells, contains two genes linked by internal ribosome entry site and
 PT controlled by target-specific regulator.
 XX Example; Page 105-106; 148pp; English.

CC The sequences given in AAH43607-22 represent sequences which may be used
 CC in the replication-competent adenoviral vector (A) of the invention.
 CC The vector contains two genes (G1, G2) that are co-transcribed as a
 CC single mRNA and under control of a heterologous, target cell-specific
 CC transcriptional regulatory element (TRE). G2 has a mutation in, or
 CC deletion of, its endogenous promoter and is controlled from an internal
 CC ribosome entry site (IRES). (A) has greater specificity for a target
 CC cell than a similar vector in which TRE is operably linked to a gene
 CC and which lacks an IRES. (A) are used to modify the genotype of target
 CC cells, optionally in vitro with subsequent return of altered cells to
 CC the host and where G2 is a cytotoxic gene, to confer selective cyto-
 CC toxicity to target cells, especially for killing cancer cells. Also
 CC (A) are used for diagnosis and monitoring, e.g. detection of bladder
 CC cancer cells. The target cell-specific TRE ensures that (A) has better
 CC targeting specificity, with minimal replication in non-target cells, so
 CC a runaway infection is prevented but production of adenoviral proteins
 CC in target cells activates and/or stimulates the immune response against
 CC target cells producing such proteins. The use of an IRES (rather than
 CC two identical control elements) eliminates the risk of homologous
 CC recombination and may provide enough extra space for an additional
 CC (therapeutic) gene.

XX Sequence 546 BP; 176 A; 96 C; 122 G; 152 T; 0 other;

Query Match 73.0%; Score 219; DB 22; Length 546;
 Best Local Similarity 99.6%; Pred. No. 3e-47;
 Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 71 ATTACTAACCTTATTGTTTAAATATTCTAACCATTAAGAAATTAACCTATTATGTTGAATAGA 130
 DB 251 ATTACTAACCTTATTGTTTAAATATTCTAACCATTAAGAAATTAACCTATTATGTTGAATAGA 310
 QY 131 GTTTTTCACCTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAATTCGAAAG-AAA 189
 DB 311 GTTTTTCACCTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAATTCGAAAGAAAA 370
 QY 190 AGTCAGTCATGTCGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAAGACTTAAAGCTTTTGTATG 249
 DB 371 AGTCAGTCATGTCGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAAGACTTAAAGCTTTTGTATG 430
 QY 250 CTGAGGTTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
 DB 431 CTGAGGTTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 9
 ID AAF87236
 XX AAF87236 standard; DNA; 546 BP.

AC AAF87236;
 XX 26-MAR-2002 (first entry)
 DT Tyrosinase-TRE fusion protein coding sequence.
 DE Tumour growth suppression; adenovirus vector; antineoplastic agent;
 XX transcriptional regulatory element; TRE; radiotherapy; bladder cancer;
 KW prostate cancer; liver cancer; breast cancer; colon cancer; melanoma;
 KW ovarian cancer; pancreatic cancer; lung cancer; brain cancer; therapy;
 KW Tyrosinase-TRE; ds.
 XX Homo sapiens.
 OS WO200172341-A2.
 PN 04-OCT-2001.
 PD 21-MAR-2001; 2001WO-US09042.
 PF 24-MAR-2000; 2000US-192015P.
 PR (CALY-) CALYDON INC.
 PA Yu D, Chen Y, Henderson DR;
 PI WPI; 2001-648426/74.
 DR Suppression of tumour growth, e.g. liver, bladder or breast cancer,
 XX comprises using a synergistic combination of adenovirus vector and
 XX antineoplastic agent or radiotherapy.
 PT Claim 12; Page 174; 248pp; English.

XX This sequence represents a Tyrosinase-TRE fusion protein coding sequence
 CC used in the scope of the invention. The invention relates to a method
 CC for the suppression of tumour growth comprising the administration of:
 CC (a) a target cell-specific adenovirus vector comprising an adenoviral
 CC gene essential for replication under transcriptional control of a
 CC target cell-specific transcriptional regulatory element (TRE); and
 CC (b) at least one antineoplastic agent; or (c) a course of radiotherapy
 CC where the amount of (a) and/or (b) or (c) is lower than that known to be
 CC effective for suppressing tumour growth when administered alone.
 CC The method is used for suppression of tumour growth for treatment of
 CC e.g. bladder cancer, prostate cancer, liver cancer, breast cancer, colon
 CC cancer, melanoma, ovarian cancer, pancreatic cancer, lung cancer or brain
 CC cancer. The combinations enhance the efficacy of treatment, allowing
 CC lower doses to be administered, reducing toxicity and suffering of the
 CC patient.

XX Sequence 546 BP; 176 A; 96 C; 122 G; 152 T; 0 other;

Query Match 73.0%; Score 219; DB 23; Length 546;
 Best Local Similarity 99.6%; Pred. No. 3e-47;
 Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 71 ATTACTAACCTTATTGTTTAAATATTCTAACCATTAAGAAATTAACCTATTATGTTGAATAGA 130
 DB 251 ATTACTAACCTTATTGTTTAAATATTCTAACCATTAAGAAATTAACCTATTATGTTGAATAGA 310
 QY 131 GTTTTTCACCTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAATTCGAAAG-AAA 189
 DB 311 GTTTTTCACCTTTAACATAGCCCTATCCCACTGGTGGGATACGAGCCAAATTCGAAAGAAAA 370
 QY 190 AGTCAGTCATGTCGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAAGACTTAAAGCTTTTGTATG 249
 DB 371 AGTCAGTCATGTCGCTTTTTCAGAGGATGAAGCTTAAAGACTTAAAGACTTAAAGCTTTTGTATG 430
 QY 250 CTGAGGTTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 300
 DB 431 CTGAGGTTGGAGTGGTATTATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 10	
AA563367/c	
ID	AAS63367 standard; DNA; 3586 BP.
XX	
AC	AAS63367;
XX	
XX	
DT	29-JAN-2002 (first entry)
XX	
XX	Chemically pretreated metabolism associated gene #62.
DE	
XX	Human; cytostatic; anti-tumour; metabolism; metabolic disease; liver;
KW	Solid tumour; cancer; cytosine methylation; epigenetic; eye; kidney;
KW	single nucleotide polymorphism detection; SNP; stool; urine; lung;
KW	cerebral-spinal fluid; intestine; brain; heart; prostate; breast;
KW	DUSP2; EPHA2; QDPR; SGSH; SHMT2; SLC7A2; SLC7A4; TYMS; ds.
XX	
OS	Homo sapiens.
XX	
WO	WO200176451-A2.
PN	
XX	18-OCT-2001.
XX	
PD	06-APR-2001; 2001WO-EP04016.
XX	
XX	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	
PA	(EPIG-) EPIGENOMICS AG.
PI	
XX	Olek A, Piepenbrock C, Berlin K;
XX	
DR	WPI; 2002-010834/01.
XX	
XX	New nucleic acid, useful for diagnosis and therapy of metabolic
PT	disease, solid tumour and cancers, comprises segment of chemically
PT	modified genomic sequences of genes associated with metabolism -
XX	
XX	Claim 1; Page 141-142; 143pp; English.
PS	
XX	The invention relates to a nucleic acid (I) comprising a sequence at
CC	least 18 bases of a segment of the chemically pretreated DNA of genes
CC	associated with metabolism such as DUSP2 (NM_004418), EPHA2 (NM_001979),
CC	QDPR (NM_000320), SGSH (NM_000199), SHMT2 (NM_005412), SLC7A2
CC	(NM_003046), SLC7A4 (NM_004173) and TYMS (NM_001071) (all
CC	undefined). (I) are useful for diagnosis and therapy of metabolic
CC	disease, solid tumours and cancers; as primer oligonucleotides for the
CC	amplification of DNA sequences, for detecting the cytosine methylation
CC	state and/or single nucleotide polymorphisms (SNPs) in a chemically
CC	treated DNA of genes associated with metabolism. An array of (I) is
CC	useful for ascertaining genetic and/or epigenetic parameters for the
CC	diagnosis and/or therapy of existing diseases or the predisposition to
CC	specific diseases by analysing cytosine methylations. The method involves
CC	chemically treating genomic DNA sample by a solution of bisulphite,
CC	hydrogen sulphite or disulphite such that cytosine bases which are
CC	unmethylated at the 5th-position are converted to uracil or another base
CC	which is dissimilar to cytosine in terms of hybridisation behaviour and
CC	amplifying fragments of the chemically pretreated genomic DNA. The
CC	genomic DNA is from cells or cellular components which contain DNA,
CC	sources of DNA comprising, for e.g. cell lines, biopsies, blood, sputum,
CC	stool, urine, cerebral-spinal fluid, tissue embedded in paraffin such as
CC	tissue from eye, intestine, kidney, brain, heart, prostate, lung, breast
CC	or liver, histologic object slides and their combinations. Genetic
CC	parameters are mutations, in particular insertions, deletions, point
CC	mutations, inversions and polymorphisms of genes associated with
CC	metabolism and sequences further required for their regulation.
CC	Epigenetic parameters are in particular cytosine methylations and
CC	further chemical modifications of DNA bases of genes associated with
CC	metabolism. Further epigenetic parameters include for e.g. the
CC	acetylation of histones which correlates with DNA methylation.
CC	AAS63306-AA563373 represent chemically pretreated metabolism associated
CC	genes, and related primers of the invention.

XX SQ Sequence 3586 BP; 1063 A; 22 C; 636 G; 1865 T; 0 other;
Query Match 67.5%; Score 202.4; DB 24; Length 3586;
Best Local Similarity 79.7%; Pred. No. 8.5e-43;
Matches 239; Conservative 0; Mismatches 61; Indels 0; Gaps

QY 1 TCATTGCCAAGGTCAAATCATCATAGTTTGTGTAAGTCTATTAACTGGGTTTCTTAGGTC 60
DB 2979 TCATTACAAAATCAAATCATCATAGTTTGTGTAAGTCTATTAACTGGGTTTCTTAGGTC 60
QY 61 AGCATTATATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 120
DB 2919 AAACATTATATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 120
QY 121 GGTGAATAGAGTTTTCACCTTTAACTAGGCTATCCCACTGGTGGGATCGAGCCCAATT 180
DB 2859 AATAAATAAAATTTTTCACCTTTAACTAGGCTATCCCACTGGTGGGATCGAGCCCAATT 180
QY 181 CGAAAGAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAAGATAAAGATAAAG 240
DB 2799 CGAAAGAAAGTCAGTCATGCTCTTTCAGAGGATGAAGCTTAAGATAAAGATAAAG 240
QY 241 TGTTCATGCTGGAGTGGGAGTGGTATATATAGTCTCAGCAAGACATGTCTAATC 300
DB 2739 TATTTAATACTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 300

RESULT 11
AAQ58032
ID AAQ58032 standard; DNA; 4752 BP.
XX
XX AAQ58032;
XX
XX
DT 01-AUG-1994 (first entry)
XX
DE Tyrosinase promoter.
XX
XX Tyrosinase; cytokine; tumor therapy; gene therapy; melanoma;
KW B16; tumor-specific promoter; polymerase chain reaction; PCR;
KW B16; primer; ds.
XX
XX
OS Mus sp.
XX
XX WO9404196-A.
XX
XX
PD 03-MAR-1994.
XX
PF 16-AUG-1993; 93WO-CB01730.
XX
PR 14-AUG-1992; 92GB-0017270.
PR 27-FEB-1993; 93GB-0004024.
XX
XX (IMCR) IMPERIAL CANCER RES TECHNOLOGY.
PA
XX
XX Hart IR, Wile RG;
PI
XX
XX
XX WPI; 1994-082848/10.
XX
PT DNA construct encoding cytokine for expression in tumour cells -
PT for treating melanoma, pancreatic, breast, colon, prostate cancer
XX
XX Disclosure; Page 67-70; 107pp; English.
XX
CC Cytokine genes are expressed in tumor cells, especially melanoma
CC cells, under the control of the tumor-specific tyrosinase gene
CC promoter, for gene therapy. A DNA fragment from the 5' end of
CC the tyrosinase gene was generated by PCR from genomic DNA of the
CC B16 melanoma line using the primers given in AAQ58041-46.
XX
XX Sequence 4752 BP; 1550 A; 854 C; 883 G; 1465 T; 0 other;
SQ

Query Match 22.3%; Score 67; DB 15; Length 4752;

[illegible]

Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, aging, glomerular disease, Lewy body disease, arthritis, arteriosclerosis, solid tumours and cancers.

Seq	Sequence	7195 BP:	2059 A;	224 C;	1725 G;	3187 T;	0 other:
Query Match	13.6%	Score	40.8;	DB	22;	Length	7195;
Best Local Similarity	48.3%;	Pred. No.	0.52;				
Matches	114;	Conservative	0;	Mismatches	122;	Indels	0;
Gaps	0;						

Qy	13	TCAATCATCATTAAGTTTGTGAGTCTATTAACTGGGTTTGGCTTAGGTCAGGCATTATTAT	72
Db	2750	TTAAAGTGTATTGGTTTGAAGAAATTTATTTTGTGTAGTTAGATTATGTCGCTTTT	2809
Qy	73	TACTAACTTATTGTTTAATATPCTAACCATTAAGAAATTAACATATTAAATGGTGAATAGAGT	132
Db	2810	TTTTTAGTTTAAAAATAAATTTAGTTGAAAAGCTAAATAATAAATATTTTATGATATAGATT	2869
Qy	133	TTTTCACCTTTAAACATAGGCCCTATCCCACTGGTGGGATACGAGCCCAATTCGAAGAAAAGT	192
Db	2870	AATAATAAAAATAAGAAGGTAATTTGTTGGTGTTAGATATTGTNATAAGTTAAATAAGT	2929
Qy	193	CAGTCATGTGCTTTTTCAGAGGATGAAAGCTTTAAGATAAAGACTAAAAGCTGTTTGGAT	248
Db	2930	AATTTTGTGTGAATATTGAAGTAAGTCTTTTGAAGAAATTTATAAAGCTTTATGAT	2985

RESULT	14
ABK28165	ABK28165 standard; DNA; 7195 BP.
ID	ABK28165
XX	AC
XX	AC
XX	ABK28165;
XX	
23-APR-	2002 (first entry)
DE	DNA transcription associated genomic DNA #20.
DE	
XX	DNA transcription associated gene; peptide nucleic acid; PNA-oligomer;
XX	PNA; cytosine methylation state; SNP; retroviral infection; gene; ds;
KW	single nucleotide polymorphism; adenosine deaminase deficiency; cancer;
KW	viral infection; Sezary syndrome; haematological disorder; tuberculosis;
KW	immunological disorder; Werner syndrome; developmental disorder;
KW	psoarosis; Rieger's syndrome; neurological disorder; erythropoietis;
KW	neurodegenerative disorder; Waardenburg syndrome; Niemann-Pick disease;
KW	myelodysplastic syndrome; myocardial infarction; hypertension; arthritis
KW	angiogenesis; congenital heart disease; HDR syndrome; gene therapy;
KW	polyglutamine disorder; solid tumour.

XX	Unidentified.
OS	
XX	WO200192565-A2.
XX	
PN	
XX	
XX	06-DEC-2001.
PD	
XX	
XX	06-APR-2001; 2001WO-EP03973.
PF	
XX	
XX	06-APR-2000; 2000DE-1019058.
PR	
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
PR	
XX	

PA (EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Berlin K;

WPI: 2002-090046/12.

New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer -

Claim 1: SEO ID No 39; 32pp; English.

The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer, in particular an oligonucleotide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, haematological disorders, immunological disorders, Werner syndrome, tuberculosis, developmental disorders, psoriasis, Rieger's syndrome, neurological disorders, neurodegenerative disorders, Waardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial infarction, hypertension, angiogenesis, erythropoiesis, congenital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABK28472 represent DNA transcription associated genomic DNA molecules of the invention.

CC associated genomic DNA molecules of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format directly from the
CC European Patent Office.

Sequence 7195 BP; 2059 A; 224 C; 1725 G; 3187 T; 0 other;

Query Match 13.6%; Score 40.8; DB 24; Length 7195;
Best Local Similarity 48.3%; Pred. NO. 0.52;
Matches 114; Conservative 0; Mismatches 122; Indels 0; Gaps 0;

Qy	13	TCAAATCATCATTAGTTTTGTAGCTATTAACTGGGTTTGCTTACGTCAGGCATTATTAT	72
Db	2750	TAAATCTTTATTTGGTTTATGAAATTTTATTTTGTAGTTAGATTATGTCGCTTTTT	2809
Qy	73	TACTAACCTTTATTGTTTAATATCTACCATAGAAATTTAACTATTAAATGGTCAATAGAGT	132
Db	2810	TTTTTAGTTTTAAATAAATTTAGTTGAAAGTAATAATAATATTATTATGTATATAGATT	2869
Qy	133	TTTTTCACCTTTAAACATAGGCCTATCCACATGGTGGGATACGAGCCAAATTCGAAAGAAAGT	192
Db	2870	AATAATAAAAAATAGAAGTAATTGTTTGGTGTAGATATTGTAATAAGTTAATAAGT	2929
Qy	193	CAGTCATGTGCTTTTCAGAGGATGAAGCTTAAGATAAAGACATAAAGCTGTTTCAAT	248
Db	2930	AATTTTGTCTAAATATTGAAGTAAGCTGTTTGAAGAAATTTATAAAGATTATATCAT	2985

RESULT 15

AAS60958
 ID AAS60958 standard: CDNA: 2041 BP

XX
AC AAS60958:XX
DT 29-JAN-2002 (first entry)-

Human cancer agent-resistance marker #617.

Human; cancer cell marker; TAXOL; cytostatic; tumour; carcinoma;
 KW squamous cell carcinoma; sarcoma; fibrosarcoma; leukaemia;
 KW lymphocytic leukaemia; lymphoma; plasmacytoma; reticulum cell sarcoma
 KW Hodgkin's disease; glioma; ss.

```
XX OS Homo sapiens.
XX PN WO200179556-A2.
XX PD 25-OCT-2001.
XX PF 13-APR-2001; 2001WO-US12132.
XX PR 14-APR-2000; 2000US-197538P.
XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX PI Lillie J, Brown JL, Bolt A, Van Huffel C;
XX DR WPI; 2001-602933/68.
XX PT Novel nucleic acid, used as a marker to determine the effectiveness of
XX using TAXOL to treat cancer cell growth in individuals -
XX PS Claim 1; Page 460-461; 527pp; English.
XX The invention relates to 1046 novel nucleic acids which are used as
CC markers for determining the sensitivity of a cancer cell to the
CC anticancer agent TAXOL. Cancer cells can be treated with TAXOL when
CC they are shown to express one of the 242 sensitivity markers or the
CC cells are shown not to express one of the 804 resistance markers.
CC The methods can be used to determine the effectiveness of TAXOL
CC in the treatment of cancer cell growth in an individual. The markers
CC can be used as targets in developing anti-cancer agents such as
CC chemotherapeutic compounds. The markers can also be used as targets in
CC developing treatments for cancer, particularly those cancers which
CC display resistance to agents and exhibit expression of the markers. The
CC anticancer agents developed by the novel method can be used to treat
CC cancer. Probes based on the markers can be used to detect transcripts or
CC genomic sequences corresponding to the markers, in the identification of
CC cells or tissues which mis-express the protein. Cancers which may
CC be targeted include carcinoma (e.g. squamous cell carcinoma),
CC sarcoma (e.g. fibrosarcoma) leukaemia (e.g. lymphocytic leukaemia),
CC lymphoma, plasmocytoma, reticulum cell sarcoma, Hodgkin's disease and
CC tumours (e.g. glioma). The present sequence is one of the 1046
XX novel cancer cell markers.
XX SQ Sequence 2041 BP; 564 A; 467 C; 455 G; 548 T; 7 other;
Query Match 13.3%; Score 40; DB 22; Length 2041;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 261 ACTGGTATTATAGTCTCAGCCAGACATGTGATAATC 300
DB 7 ACTGGTATTATAGTCTCAGCCAGACATGTGATAATC 46
Search completed: May 10, 2003, 16:18:04
Job time : 273 secs
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GenCore version 5.1.4.p5_4578
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OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 16:13:41 ; Search time 70 Seconds
(without alignments)
1314.329 Million cell updates/sec

Title: US-09-721-391-1

Perfect score: 300

Sequence: 1 tcatttgcaagtcacaaatca.....agccaagacatgtgataatc 300

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued_Patents_NA:**
- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:**
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:**
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:**
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:**
- 5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq:**
- 6: /cgn2_6/ptodata/1/ina/backfiles.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	300	100.0	2384	1 US-08-181-471-1	Sequence 1, Appli
2	300	100.0	2384	4 US-09-056-105-3	Sequence 3, Appli
3	289	96.3	2397	1 US-07-891-942G-11	Sequence 11, Appli
C 4	34.6	11.5	1001	4 US-09-641-638-377	Sequence 377, App
C 5	34.2	11.4	1725	4 US-09-134-001C-2572	Sequence 2572, Ap
6	34.2	11.4	3155	2 US-08-591-629-7	Sequence 7, Appli
7	33.8	11.3	1512	4 US-09-134-001C-1111	Sequence 1111, Ap
C 8	33.4	11.1	1001	4 US-09-641-638-376	Sequence 376, App
9	32.4	10.8	334	2 US-09-032-684-8	Sequence 8, Appli
10	32.2	10.7	2048	1 US-08-416-870C-7	Sequence 7, Appli
11	32.2	10.7	3696	2 US-08-657-641-4	Sequence 4, Appli
12	32.2	10.7	3696	5 PCT-US94-07233-4	Sequence 4, Appli
C 13	32.2	10.7	5303	4 US-08-971-395-4	Sequence 4, Appli
C 14	32	10.7	2476	4 US-08-844-274-11	Sequence 11, Appl
15	32	10.7	4198	4 US-09-586-719-11	Sequence 11, Appl
16	32	10.7	5194	4 US-08-844-274-16	Sequence 16, Appl
17	32	10.7	5194	4 US-08-844-274-17	Sequence 17, Appl
C 18	32	10.7	5679	4 US-08-844-274-10	Sequence 10, Appl
C 19	32	10.7	6448	4 US-08-844-274-15	Sequence 15, Appl
C 20	32	10.7	6723	4 US-08-844-274-13	Sequence 13, Appl
21	32	10.7	6723	4 US-08-844-274-14	Sequence 14, Appl
C 22	32	10.7	7560	4 US-08-844-274-20	Sequence 20, Appl
C 23	31.8	10.6	9060	4 US-08-378-313-20	Sequence 20, Appl
24	31.8	10.6	84495	4 US-09-797-906-3	Sequence 3, Appli
C 25	31.6	10.5	263	3 US-08-765-332-144	Sequence 144, App
C 26	31.6	10.5	263	4 US-09-448-894-144	Sequence 144, App
C 27	31.6	10.5	2237	4 US-08-914-999-7	Sequence 7, Appli

28	31.4	10.5	4285	4 US-09-410-464-1	Sequence 1, Appli
C 29	31.4	10.5	8920	2 US-08-446-855A-1	Sequence 1, Appli
C 30	31.4	10.5	8920	4 US-09-150-741-1	Sequence 1, Appli
C 31	31.2	10.4	4291	2 US-08-417-210A-81	Sequence 81, Appli
32	31	10.3	750	2 US-08-687-080-74	Sequence 74, Appli
C 33	31	10.3	1546	3 US-08-961-083-21	Sequence 21, Appli
C 34	31	10.3	6854	4 US-09-066-047-6	Sequence 6, Appli
35	30.8	10.2	4285	4 US-09-410-464-1	Sequence 1, Appli
C 36	30.6	10.2	4285	4 US-09-410-464-1	Sequence 1, Appli
C 37	30.6	10.2	5300	1 US-08-765-014-1	Sequence 3, Appli
38	30.6	10.2	6124	4 US-08-213-419B-3	Sequence 3, Appli
39	30.6	10.2	12571	4 US-09-322-478-20	Sequence 20, Appli
C 40	30.4	10.1	7336	4 US-09-306-446C-1	Sequence 1, Appli
C 41	30.2	10.1	1524	4 US-09-134-001C-2234	Sequence 2234, Ap
42	30.2	10.1	1680	4 US-08-961-527-270	Sequence 270, App
43	30	10.0	30	4 US-09-150-766-14	Sequence 14, Appli
44	30	10.0	211	1 US-07-593-657-12	Sequence 12, Appli
45	30	10.0	1388	1 US-08-282-581-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-08-181-471-1
; Sequence 1, Application US/08181471
; Patent No. 5641508
; GENERAL INFORMATION:
; APPLICANT: Li, Lingna
; APPLICANT: Lishko, Valeryi K.
; TITLE OF INVENTION: METHOD FOR DELIVERING BENEFICIAL
; TITLE OF INVENTION: COMPOSITIONS TO HAIR FOLLICLES
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Thomas Fitting
; STREET: 12526 High Bluff Drive, Suite 300
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92130
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/181,471
; FILING DATE: 13-JAN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/041,553
; FILING DATE: 02-APR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitting, Thomas
; REGISTRATION NUMBER: 34,163
; REFERENCE/DOCKET NUMBER: ANT0029P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-792-3680
; TELEFAX: 619-792-8477
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 503..2092
US-08-181-471-1

Query Match 100.0%; Score 300; DB 1; Length 2384;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 124 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 183
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 120
DB 184 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 243
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 303
QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 363
QY 241 TCTTTGATCGTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAATC 300
DB 364 TCTTTGATCGTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAATC 423

RESULT 2
US-09-056-105-3
; Sequence 3, Application US/09056105
; Patent No. 6287569
; GENERAL INFORMATION:
; APPLICANT: KIPPS, THOMAS J.
; APPLICANT: WU, YUNQI
; TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR
; FILE REFERENCE: 233/221
; CURRENT APPLICATION NUMBER: US/09/056.105
; EARLIER FILING DATE: 1998-04-06
; EARLIER FILING DATE: 1997-04-10
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-056-105-3

Query Match 100.0%; Score 300; DB 4; Length 2384;
Best Local Similarity 100.0%; Pred. No. 2.7e-77;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 124 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 183
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 120
DB 184 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 243
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 244 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 303
QY 181 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 240
DB 304 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAAG 363
QY 241 TCTTTGATCGTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAATC 300
DB 364 TCTTTGATCGTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAATC 423

RESULT 3

US-07-891-942G-11
; Sequence 11, Application US/07891942G
; Patent No. 5679511
; GENERAL INFORMATION:
; APPLICANT: Kwon, Byoung Se
; TITLE OF INVENTION: CDNA CLONES FOR HUMAN TYROSINASE AND FOR
; TITLE OF INVENTION: A REGULATORY PROTEIN IN THE MELANIN PROTEIN PATHWAY
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christopher A. Michaels, Barnard, Brown &
; ADDRESS: Michaels
; STREET: 306 East State Street; Suite 220
; CITY: Ithaca
; STATE: NY
; COUNTRY: USA
; ZIP: 14850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/891,942G
; FILING DATE: 01-JUN-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 06/915,753
; FILING DATE: 06-OCT-1986
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/362,847
; FILING DATE: 07-JUN-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Michaels, Christopher A
; REGISTRATION NUMBER: 34,390
; REFERENCE/DOCKET NUMBER: IND1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 607-273-1711
; TELEFAX: 607-273-2609
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2397 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-891-942G-11

Query Match 96.3%; Score 289; DB 1; Length 2397;
Best Local Similarity 99.7%; Pred. No. 3.9e-74;
Matches 300; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 60
DB 1936 TCATTGCAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTGCTTAGGTC 1985
QY 61 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 120
DB 1986 AGGCATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAATAAATTAAT 2045
QY 121 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 180
DB 2046 GGTGAATAGAGTTTTCACCTTAAACATAGGCTATCCCACTGGTGGGATACAGCAATT 2105
QY 181 CGAAG-AAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAA 239
DB 2106 CGAAGAAAAGTCAGTCATGTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAA 2165
QY 240 GTGTTTGTATGCTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAAT 299
DB 2166 GTGTTTGTATGCTGGAGGTGGGAGTGGTATTATATAGGCTTCAGCCCAAGACATGTGATAAT 2225

QY 300 C 300


```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 93202425.0
; FILING DATE: 17-AUG-93
; ATTORNEY/AGENT INFORMATION:
; NAME: MASS, CLIFFORD J.
; REGISTRATION NUMBER: 30.086
; REFERENCE/DOCKET NUMBER: U-010627-0
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 708-1800
; TELEFAX: (212) 246-8959
; TELEX: 233288
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3155 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Nicotiana tabacum
; STRAIN: Samsun NN
; FEATURE:
; NAME/KEY: exon
; LOCATION: 454..907
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1859..2497
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2847..2884
; FEATURE:
; NAME/KEY: intron
; LOCATION: 908..1858
; FEATURE:
; NAME/KEY: intron
; LOCATION: 2498..2846
; NAME/KEY: CDS
; LOCATION: join(454..907, 1859..2497, 2847..2884)
US-08-591-629-7

Query Match
Best Local Similarity 11.4%; Score 34.2; DB 2; Length 3155;
Matches 60; Conservative 0; Mismatches 43; Indels 0; Gaps 0;

QY 65 ATTATTACTAACTTATCTTAAATTCCTAAGCAATGAAGTAACTATTAACTGTTG 124
|||||
DB 2736 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 2795
|||||

QY 125 AATAGAGTTTTTCACTTTAACTATAGCGCTATCCCACTGGTGG 167
|||||
DB 2796 ATTATTATTATTATTATTATTATTATTATTATTACATTTCCCACTGTTGG 2838
|||||

RESULT 7
US-09-134-001C-1111
; Sequence 1111, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1111
; LENGTH: 1512

; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1111

Query Match
Best Local Similarity 11.3%; Score 33.8; DB 4; Length 1512;
Matches 71; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 23 ATTAGTTTGTAGTCTATTAACTGGTTGCTTAGGTGAGGCATTATTATTTCACTT 82
|||||
DB 1261 ATTGTTTATATTATTACGCATCATTTATTTCTTCAGACATTAAGTAAGCTTATATTTCAT 1320
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QY 83 ATTGTTATATTTCTAACCATAGAACTAATTAAGTAACTATTAAATGGTCAATAGAGTTTTCACATT 142
|||||
DB 1321 ATTGTTTCCACCACCATCATAGTATTATTTCTATCGATGCTATTATATTATTTTCGGCAGT 1380
|||||

QY 143 AACATAGGCCTAT 155
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DB 1381 ATGTTAAGCATAT 1393
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RESULT 8
US-09-641-638-376/C
; Sequence 376, Application US/09641638
; Patent No. 6432848
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GENSET.051CPI
; CURRENT APPLICATION NUMBER: US/09/641.638
; CURRENT FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 376
; LENGTH: 1001
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 501
; OTHER INFORMATION: 12-878-153 : polymorphic base C or T
; NAME/KEY: misc.binding
; LOCATION: 481..500
; OTHER INFORMATION: 12-878-153.mis1, potential
; NAME/KEY: misc.binding
; LOCATION: 502..521
; OTHER INFORMATION: 12-878-153.mis2, potential complement
; NAME/KEY: primer.bind
; LOCATION: 349..369
; OTHER INFORMATION: upstream amplification primer
; NAME/KEY: primer.bind
; LOCATION: 839..859
; OTHER INFORMATION: downstream amplification primer, complement
; NAME/KEY: misc.binding
; LOCATION: 489..513
; OTHER INFORMATION: 12-878-153 potential probe
; US-09-641-638-376

Query Match
Best Local Similarity 11.1%; Score 33.4; DB 4; Length 1001;
Matches 70; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
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RESULT 10
US-08-416-870C-7
; Sequence 7, Application US/08416870C
; Patent No. 5824862
; GENERAL INFORMATION:

RESULT 11
US-08-657-641-4
; Sequence 4, Application US/08657641
; Patent No. 5945277
; GENERAL INFORMATION:
; APPLICANT: Nichol, Stuart T.
; APPLICANT: Spiropoulou, Christina
; APPLICANT: Kislazek, Thomas G.
; APPLICANT: Rollin, Pierre E.
; TITLE OF INVENTION: NUCLEIC ACID
; TITLE OF INVENTION: AND
; TITLE OF INVENTION: REAGENTS FOR
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Suite 1200, The Canal
; STREET: 127 Peachtree Street,
;

CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303-1811
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,641
FILING DATE: 24-JUN-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/133,591
FILING DATE: 07-OCT-1993
APPLICATION NUMBER: US 1414,074
FILING DATE: 24-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perryman, David G.
REGISTRATION NUMBER: 33,438
REFERENCE/DOCKET NUMBER: 1414,089
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-688-0770
TELEFAX: 404-688-9880
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hantavirus
STRAIN: New
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M Segment
UNITS: 3696 BP
US-08-657-641-4

Query Match 10.7% Score 32.2; DB 2; Length 3696;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 8 CAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGTCTTAGGTACGGCATT 67
DB 3502 CAACATTATTTTCATTATATGTATGTTCTTATATCAATAACATTTGTATATATCCCATACC 3561
QY 68 ATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATTAACCTATTATGTTGAAT 127
DB 3562 GAAATATTATACATAATTTTATTTTATACAAAGTATTAACTAACCCATTAAACAGCTAAA 3621
QY 128 AGAGTTTTTTCACCTTTAACATAGGCTATCCCACTGGTGGATACAGCAATT 180
DB 3622 AAAACAATCCTTAACACCTATATATATCCCATTTGCTTATTACGAGGCTTTT 3674

RESULT 12
PCT-US94-07233-4
Sequence 4, Application PC/TUS9407233
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: NUCLEIC ACIDS OF A NOVEL HANTAVIRUS AND REAGENTS FOR DETECTION
NUMBER OF SEQUENCES: 12
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07233

FILING DATE: 24-JUN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/084,724
FILING DATE: 24-JUN-1993
APPLICATION NUMBER: US 08/591,133
FILING DATE: 07-OCT-1993
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3696 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Nucleic Acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Hantavirus
STRAIN: New
POSITION IN GENOME:
CHROMOSOME/SEGMENT: M Segment
UNITS: 3696 BP
PCT-US94-07233-4
Query Match 10.7% Score 32.2; DB 5; Length 3696;
Best Local Similarity 49.1%; Pred. No. 3;
Matches 85; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 8 CAAGGTCAAAATCATCATAGTTTGTAGTCTATTAACTGGGTTTGTCTTAGGTACGGCATT 67
DB 3502 CAACATTATTTTCATTATATGTATGTTCTTATATCAATAACATTTGTATATATCCCATACC 3561
QY 68 ATTATTACTAACCTTATTGTTAAATTTCTAACCATTAAGAAATTAACCTATTATGTTGAAT 127
DB 3562 GAAATATTATACATAATTTTATTTTATACAAAGTATTAACTAACCCATTAAACAGCTAAA 3621
QY 128 AGAGTTTTTTCACCTTTAACATAGGCTATCCCACTGGTGGATACAGCAATT 180
DB 3622 AAAACAATCCTTAACACCTATATATATCCCATTTGCTTATTACGAGGCTTTT 3674

RESULT 13
US-08-971-395-4/c
Sequence 4, Application US/08971395
Patent No. 6359197
GENERAL INFORMATION:
APPLICANT: Amasino, Richard M
APPLICANT: No. 6359197, Yoo-Sun
APPLICANT: Gan, Susheng
TITLE OF INVENTION: Transgenic Plants with Altered Senescence Characteristics
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/971,395
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.94908
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000

TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-971-395-4

Query Match 10.7%; Score 32.2; DB 4; Length 5303;
Best Local Similarity 52.6%; Pred. No. 3.3;
Matches 70; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
Qy 4 TTGCAAGTCGAATCATATAGTTTCTAGTCTATTAACTGGGTTTCTTAGGTCAGG 63
Db 648 TTAACATATCTCAATAAAGTAATAGGTATCCATCTTTTGGGTTGTTTCGTCTAAG 589
Qy 64 CATTATATTACTAACCTTATTGTTAAATATCTAACCATPAAGAAATTAACATTAATGCT 123
Db 588 TAGTATTTTTTTAGAAATTTTGATAATCTTAAACTAAAGATAATTAATATTTTAAAGT 529
Qy 124 GAATAGAGTTTTT 136
Db 528 ATATAAATTTGTAT 516

RESULT 14
US-08-844-274-11
Sequence 11, Application US/08844274B
Patent No. 6218185
GENERAL INFORMATION:
APPLICANT: Fraser Jr., Malcom J.
APPLICANT: Shirk, Paul D.
APPLICANT: Ellick, Teri A.
APPLICANT: Perera, Omathage
TITLE OF INVENTION: PiggyBac Transposon-Based Genetic Transformation System
FILE REFERENCE: 0148.96
CURRENT APPLICATION NUMBER: US/08/844,274B
EARLIER FILING DATE: 1997-04-18
EARLIER FILING DATE: 1996-04-19
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0 - beta
SEQ ID NO 11
LENGTH: 2476
TYPE: DNA
ORGANISM: Trichoplusia ni
FEATURE:
NAME/KEY: CDS
LOCATION: (333)..(2123)
US-08-844-274-11

Query Match 10.7%; Score 32; DB 4; Length 2476;
Best Local Similarity 55.4%; Pred. No. 3;
Matches 62; Conservative 0; Mismatches 50; Indels 0; Gaps 0;
Qy 16 AATCATCATAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTCAGGCATTATTATTAC 75
Db 150 AAGTGTCACGTGATTTTGAACATATAACGCCGCGTGAGTCAAAATGACGATGATTATCTT 209
Qy 76 TAACCTTATTGTTAATATTCTAACCATAAAGAAATTAACATTAATGTTGAAT 127
Db 210 TTACGTGACTTTTAAAGATTAACTCATACGATAAATTAATATTGTTATTTCAT 261

RESULT 15
US-09-586-719-11
Sequence 11, Application US/09586719
Patent No. 6294345
GENERAL INFORMATION:
APPLICANT: Zheng, Feng

APPLICANT: Levin, Joshua Z.
APPLICANT: Bauer, Michael W.
TITLE OF INVENTION: Herbicide Target Genes and Methods
FILE REFERENCE: PB/5-30909A
CURRENT APPLICATION NUMBER: US/09/586,719
CURRENT FILING DATE: 2000-06-05
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 4198
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-586-719-11

Query Match 10.7%; Score 32; DB 4; Length 4198;
Best Local Similarity 51.4%; Pred. No. 3.5;
Matches 74; Conservative 0; Mismatches 70; Indels 0; Gaps 0;
Qy 4 TTGCAAGTCGAATCATATAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTCAGG 63
Db 3601 TTTAAGAGAAATAAATATATGTTCTAGGTTGGGTCATTTAGCAACTATATATGATG 3660
Qy 64 CATTATATTACTAACCTTATTGTTAAATATTCTAACCATAAAGAAATTAACATTAATGCT 123
Db 3661 GATTATATTCTCTTATGATTGAAAAATTTGCAAGTGAGAAAAACATCATGTTTCTTCT 3720
Qy 124 GAATAGAGTTTTTTCACATTAACAT 147
Db 3721 AAGTTGTCCTCCAGTCCTCAAT 3744

Search completed: May 10, 2003, 17:06:22
Job time : 83 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 10, 2003, 17:05:02 ; Search time 119 Seconds
(without alignments)
3132.870 Million cell updates/sec

Title: us-09-721-391-1

Perfect score: 300

Sequence: 1 tcatttgcaggtcaaatca.....agccaagacatgtgataac 300

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 783854 seqs, 621352466 residues

Total number of hits satisfying chosen parameters: 1567708

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	300	100.0	300	10	US-09-822-634-2
2	219	73.0	546	9	US-10-053-886-1
3	219	73.0	546	9	US-09-814-357-10
4	219	73.0	552	9	US-10-053-886-16
5	68.6	22.9	320	9	US-10-053-886-7
6	40.8	13.6	7195	9	US-10-239-676-29
7	40	13.3	2041	10	US-09-834-975-959
8	38.6	12.9	4985	9	US-10-094-240-10
9	37	12.3	3996	9	US-10-087-464-42
10	36.6	12.2	113604	9	US-10-227-195A-1
11	36.6	12.2	113604	9	US-10-227-195A-2
12	36.4	12.1	380	10	US-09-969-373-85
13	36.4	12.1	380	10	US-09-969-373-86
14	36.4	12.1	15649	10	US-10-239-676-103
15	35.8	11.9	1200	10	US-09-887-576-772
16	35.8	11.9	2000	9	US-09-938-842A-3433
17	35.4	11.8	264	10	US-09-969-373-472
18	35.4	11.8	608	9	US-09-938-842A-3718
19	35.2	11.7	10957	9	US-10-125-540-555

20	35.2	11.7	10957	9	US-10-103-313-615	-Sequence 615, App
21	35.2	11.7	10957	10	US-09-764-870-555	Sequence 555, App
22	35.2	11.7	10957	10	US-09-764-853-903	Sequence 903, App
23	35.2	11.7	13217	9	US-10-125-540-556	Sequence 556, App
24	35.2	11.7	13217	9	US-10-103-313-616	Sequence 616, App
25	35.2	11.7	13217	10	US-09-764-870-556	Sequence 556, App
26	35.2	11.7	13217	10	US-09-764-853-904	Sequence 904, App
27	35.2	11.7	13220	9	US-10-125-540-554	Sequence 554, App
28	35.2	11.7	13220	9	US-10-103-313-614	Sequence 614, App
29	35.2	11.7	13220	10	US-09-764-870-554	Sequence 554, App
30	35.2	11.7	13220	10	US-09-764-853-902	Sequence 902, App
31	35.2	11.7	32249	9	US-09-860-670-260	Sequence 260, App
32	34.8	11.6	562	9	US-09-736-457-733	Sequence 733, App
33	34.8	11.6	562	9	US-09-902-941-733	Sequence 733, App
34	34.8	11.6	562	9	US-09-849-626-733	Sequence 733, App
35	34.8	11.6	562	9	US-10-017-754-733	Sequence 733, App
36	34.8	11.6	7906	9	US-10-239-676-97	Sequence 97, Appl
37	34.6	11.5	254	10	US-09-969-373-1027	Sequence 1027, Ap
38	34.6	11.5	2000	9	US-09-938-842A-4180	Sequence 4180, Ap
39	34.2	11.4	5917	9	US-10-087-464-9	Sequence 9, Appli
40	34	11.3	17431	9	US-10-072-349-247	Sequence 247, App
41	34	11.3	17431	10	US-09-764-855-247	Sequence 247, App
42	34	11.3	684973	10	US-09-263-959-1	Sequence 1, Appli
43	33.6	11.2	2000	9	US-09-938-842A-3423	Sequence 3423, Ap
44	33	11.0	145831	10	US-09-969-708-79	Sequence 79, Appl
45	33	11.0	145831	10	US-09-954-456-2116	Sequence 2116, Ap

ALIGNMENTS

RESULT 1
US-09-822-634-2
; Sequence 2, Application US/09822634
; Patent No. US20020150556A1
; GENERAL INFORMATION:
; APPLICANT: Vile, Richard G.
; APPLICANT: Harrington, Kevin
; APPLICANT: Bateman, Andrew
; APPLICANT: Murphy, Steven
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
; TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
; FILE REFERENCE: 07039-289001
; CURRENT APPLICATION NUMBER: US/09/822,634
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 60/193,977
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-634-2

Query Match 100.0%; Score 300; DB 10; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.4e-68;
Matches 300; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCATTTCGAAGTCAAATCATCTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC	60
DB	1	TCATTTCGAAGTCAAATCATCTAGTTTGTAGTCTATTAACTGGGTTTCTTAGGTC	60
QY	61	AGGCATTATTATTACTAACTTATTGTTAATATCTTAACCAATAAGAAATTAATAAT	120
DB	61	AGGCATTATTATTACTAACTTATTGTTAATATCTTAACCAATAAGAAATTAATAAT	120
QY	121	GCTGAATAGAGTTTTTCACTTTTAACATAGGCCCTATCCCACTGGTGGGATACGACCAAT	180
DB	121	GCTGAATAGAGTTTTTCACTTTTAACATAGGCCCTATCCCACTGGTGGGATACGACCAAT	180
QY	181	CGAAGAAAGTCAGTCATGCTCTTTTCAGAGATGAAGCTTAGATATAAGACTAAAG	240
DB	181	CGAAGAAAGTCAGTCATGCTCTTTTCAGAGATGAAGCTTAGATATAAGACTAAAG	240

Db 181 CGAAGAAAAGTCAGTCATGTCCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAG 240
Qy 241 TGTTCATGCTGGAGTGGAGTGGTATATATATAGTCTCAGCCCAAGACATGTGATAATC 300
Db 241 TGTTCATGCTGGAGTGGAGTGGTATATATATAGTCTCAGCCCAAGACATGTGATAATC 300

RESULT 2

US-10-053-886-1
; Sequence 1, Application US/10053886
; Publication No. US20030039633A1
; GENERAL INFORMATION:
; APPLICANT: De-Chao Yu
; APPLICANT: Yuanhao Yu
; TITLE OF INVENTION: Recombinant Oncolytic Adenovirus for
; FILE REFERENCE: CELL-021
; CURRENT APPLICATION NUMBER: US/10/053,886
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/814,357
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 546
; TYPE: DNA
; ORGANISM: H. sapiens
US-10-053-886-1

Query Match 73.0%; Score 219; DB 9; Length 546;
Best Local Similarity 99.6%; Pred. No. 1.9e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 130
Db 251 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 310
Qy 131 GTTTTTCACCTTTAATAGGCTATCCCACTGGTGGGATACAGCAATTCGAAAG-AAA 189
Db 311 GTTTTTCACCTTTAATAGGCTATCCCACTGGTGGGATACAGCAATTCGAAAGAAA 370
Qy 190 ACTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGATG 249
Db 371 AGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGATG 430
Qy 250 CTGGAGTGGGAGTGGTATATATAGTCTCAGCCCAAGACATGTGATAATC 300
Db 431 CTGGAGTGGGAGTGGTATATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 3

US-09-814-357-10
; Sequence 10, Application US/09814357
; Publication No. US20030068307A1
; GENERAL INFORMATION:
; APPLICANT: Yu, De-Chao
; APPLICANT: Chen, Yu
; APPLICANT: Henderson, Daniel R.
; TITLE OF INVENTION: METHODS OF TREATING NEOPLASIA
; TITLE OF INVENTION: WITH COMBINATION TARGET CELL-SPECIFIC ADENOVIRUS,
; FILE REFERENCE: 348022001600
; CURRENT APPLICATION NUMBER: US/09/814,357
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 546
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Tyrosinase-TRE
US-09-814-357-10

Query Match 73.0%; Score 219; DB 9; Length 546;
Best Local Similarity 99.6%; Pred. No. 1.9e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 130
Db 251 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 310
Qy 131 GTTTTTCACCTTTAATAGGCTATCCCACTGGTGGGATACAGCAATTCGAAAG-AAA 189
Db 311 GTTTTTCACCTTTAATAGGCTATCCCACTGGTGGGATACAGCAATTCGAAAGAAA 370
Qy 190 AGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGATG 249
Db 371 AGTCAGTCATGCTCTTTTCAGAGGATGAAGCTTAAGATAAAGACTAAAGTGTGATG 430
Qy 250 CTGGAGTGGGAGTGGTATATATAGTCTCAGCCCAAGACATGTGATAATC 300
Db 431 CTGGAGTGGGAGTGGTATATATAGTCTCAGCCCAAGACATGTGATAATC 481

RESULT 4

US-10-053-886-16
; Sequence 16, Application US/10053886
; Publication No. US20030039633A1
; GENERAL INFORMATION:
; APPLICANT: De-Chao Yu
; APPLICANT: Yuanhao Yu
; TITLE OF INVENTION: Recombinant Oncolytic Adenovirus for
; FILE REFERENCE: CELL-021
; CURRENT APPLICATION NUMBER: US/10/053,886
; CURRENT FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/814,357
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,015
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/814,351
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/192,156
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 552
; TYPE: DNA
; ORGANISM: H. sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(6)
; OTHER INFORMATION: AgeI restriction site
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (547)...(552)
; OTHER INFORMATION: AgeI restriction site
US-10-053-886-16

Query Match 73.0%; Score 219; DB 9; Length 552;
Best Local Similarity 99.6%; Pred. No. 2e-47;
Matches 230; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Qy 71 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 130
Db 252 ATTACTAACCTTATTGTTAAATATTCTAACCATAGAATAAATACTATTATGCTGAATAGA 311

Qy	131	GTTTTTCAC	TTTAACATAGCCCTATCCCACCTGCTGGGATACGAGCCAATTGCAAG-AAA	189
Db	312	GTTTTTCAC	TTTAACATAGCCCTATCCCACCTGCTGGGATACGAGCCAATTGCAAGAAAAA	371
Qy	190	AGTCAGTCA	TGTGCTTTTCAGAGGATGAAGCCTTAGATATAAGACTAAAGCTGTTTGATG	249
Db	372	AGTCAGTCA	TGTGCTTTTCAGAGGATGAAGCCTTAGATATAAGACTAAAGCTGTTTGATG	431
Qy	250	CTGGAGTGG	GACTGGTATTATATAGTCTCACCGCAAGACATGTGTAATC	300
Db	432	CTGGAGTGG	GACTGGTATTATATAGTCTCACCGCAAGACATGTGTAATC	482

RESULT 5

```

US-10-053-886-7
: Sequence 7, Application US/10053886
: Publication No. US20030039633A1
: GENERAL INFORMATION:
: APPLICANT: De-Chao Yu
: APPLICANT: Yuanhao Yu
: TITLE OF INVENTION: Recombinant Oncolytic
: TITLE OF INVENTION: Human Melanoma
: FILE REFERENCE: CELL-021
: CURRENT APPLICATION NUMBER: US/10/053,886
: CURRENT FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 09/814,357
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/192,015
: PRIOR FILING DATE: 2000-03-24
: PRIOR APPLICATION NUMBER: 09/814,351
: PRIOR FILING DATE: 2001-03-21
: PRIOR APPLICATION NUMBER: 60/192,156
: PRIOR FILING DATE: 2000-03-24
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 320
: TYPE: DNA
: ORGANISM: M. musculus
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (1)...(6)
: OTHER INFORMATION: XhoI restriction site
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: (315)...(320)
: OTHER INFORMATION: EagI restriction site
: US-10-053-886-7

```

Query Match 22.9%; Score 68.6; DB 9; Length 320;
Best Local Similarity 58.0%; Pred. No. 1.7e-08;
Matches 142; Conservative 0; Mismatches 99; Indels 4; Gaps 1;

Qy	56	AGGTGAGCAATTATTATTACTAACCTTATGTTAAATATTC	TACCATAGAATTAACCTA	115
Db	40	AGATGATGATATCTTGATACCTCTCTCAATTCGAAATTC	CAATTAATTAATTTTCATA	99
Qy	116	TTAATGGTGAATAGAGTTTTTCTACTTAAACATAGGGCT	TCCCACTGGTGGGATACGAGC	175
Db	100	TCAATTAGATAATATATCTCCTT---	CAATTAGTACCTACTATGGGCTATGTAC	155
Qy	176	CAATTCGAAGAAAGTCAGTCATGTGCTTTTCAGAGGAT	GAAAGCTTAAGATAAAGACT	235
Db	156	AAACTCCAGAAAAGTTAGTCATGTGCTTTGCAGAGAT	AAAGCTTAGTGTAACACAG	215
Qy	236	AAAAGCTTTTGATGCTGGAGGTGGGAGTGGTATTAT	TATAGGTCCTCAGCCAAACACATGTGA	295
Db	216	GCTGAGAGTATTGATGTAGAGAGGGAGTGGTTAT	TATAGGTCCTAGCCAAACATGTGA	275
Qy	296	TAATC	300	
Db	276	TAGTC	280	

RESULT 6

```

US-10-239-676-29
; Sequence 29, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PC/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 29
; LENGTH: 7195
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated gene
US-10-239-676-29

```

Query Match	13.6%	Score 40.8;	DB 9;	Length 7195;
Best Local Similarity	48.3%;	Pred. No. 1;		
Matches 114;	Conservative	0;	Mismatches 122;	Indels 0;
Gaps	0;			

Qy	13	TCAATCATCATNTAGTTTTGTAGCTATTAACCTGGGTTTGCTAGGTCAGGCATTAATAT	72
Db	2750	TTAAATGTTTATGGTTTGAAGATTTATTTTTTTGTTAGTATAGATTGGTCGTTTTT	2809
Qy	73	TACTAACCTTATTGTTTAATATCTACCCATAAGAATTAAAGCTATTAAATGGTGAATAGAGT	132
Db	2810	TTTTTAGTTTAAAAATAAATTTAGTTGAAAGCTAAATAAATAATTTTATCTATATAGATT	2859
Qy	133	TTTTTCACCTTAACATAGGCCTATCCACCTGGTGGGATACGAGCCAATTCGAAAT	192
Db	2870	AATAATAAAAAATAGAAAGCTAATTTGTTGGGTGTATATTTGTAATAAGTTAAATAAGT	2929
Qy	193	CAGTCATGTGCTTTTCAGAGGATGAAGCCTTAAGATAAAGACTAAAGCTGTTTGAT	248
Db	2930	AATTTTTGTGTAATAATTCGAAGTAACTGTTTTGAAGAAATTTATAAAGCTTATCAT	2985

RESULT 7

```

RES001
US-09-834-975-959
; Sequence 959, Application US/09834975
; Patent No. US20020110815A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Brown, Jeffrey
; APPLICANT: Bolt, Andrew
; APPLICANT: Van Huffel, Christophe
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
; TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAP
; TITLE OF INVENTION: OF HUMAN CANCERS
; FILE REFERENCE: MRI-016B
; CURRENT APPLICATION NUMBER: US/09/834,975
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/197,538
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 1046
; SOFTWARE: FastSeq for Windows Version 4.0

```

```
; SEQ ID NO 959
; LENGTH: 2041
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2041)
; OTHER INFORMATION: n = A,T,C or G
US-09-834-975-959

Query Match      13.3%   Score 40;   DB 10;   Length 2041;
Best Local Similarity 100.0%;   Pred. No. 0.98;
Matches 40;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy 261 AGTGGTATTATATAGGCTCTAGCCCAAGACATGTGATATC 300
      |||||
Db 7 AGTGGTATTATATAGGCTCTAGCCCAAGACATGTGATATC 46

RESULT 8
US-10-094-240-10
; Sequence 10, Application US/10094240
; Publication No. US20030082637A1
; GENERAL INFORMATION:
; APPLICANT: ZWIEBEL, LAURENCE J.
; TITLE OF INVENTION: ARRESTIN GENE, POLYPEPTIDE, AND METHODS OF USE THEREOF
; FILE REFERENCE: N8289
; CURRENT APPLICATION NUMBER: US/10/094,240
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 10/056,405
; PRIOR FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/264,649
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 10
; LENGTH: 4985
; TYPE: DNA
; ORGANISM: Anopheles gambiae
US-10-094-240-10

Query Match      12.9%   Score 38.6;   DB 9;   Length 4985;
Best Local Similarity 56.8%;   Pred. No. 3.3;
Matches 71;   Conservative 0;   Mismatches 54;   Indels 0;   Gaps 0;

Qy 17 ATCATCAATAGTTTGTAGTCTATTAACTGGTTTGTCTAGGTCAGGCATTATTATTACT 76
      |||||
Db 2561 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 2620

Qy 77 AACCTTATTGTTAATATCTCAACCATAGAATTAACCTAATTAATGGTGAATAGAGTTTTT 136
      |||||
Db 2621 ATTATTATTATTATTATTATAACAATAATAATTATTATTATTATTATTATTATTATT 2680

Qy 137 CACTT 141
      |||
Db 2681 AATTT 2685

RESULT 9
US-10-087-464-42/C
; Sequence 42, Application US/10087464
; Publication No. US20030059436A1
; GENERAL INFORMATION:
; APPLICANT: Chishti, Athar
; APPLICANT: Oh, Steven
; APPLICANT: Liu, David
; APPLICANT: Goel, Vikas
; APPLICANT: Li, Xuerong
; TITLE OF INVENTION: Band 3 Antigenic Peptides, Malaria Polypeptides and Uses Thereof
; FILE REFERENCE: S1237/7019
; CURRENT APPLICATION NUMBER: US/10/087,464
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 06/272,930

; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 42
; LENGTH: 3996
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
US-10-087-464-42

Query Match      12.3%   Score 37;   DB 9;   Length 3996;
Best Local Similarity 54.9%;   Pred. No. 7.8;
Matches 73;   Conservative 0;   Mismatches 60;   Indels 0;   Gaps 0;

Qy 15 AATCATCATAGTTTGTGTAGTCTATTAACTGGTTTGTCTAGGTCAGGCATTATTATTA 74
      |||||
Db 3647 ACATTTTCATTATTATCAACTGAAAAATCATTTATTTTAAATTCATTTTTCAGAA 3588

Qy 75 CTAACCTTATTGTTAAATATTCTAACCATAGAATTAACCTAATTAATGGTGAATAGAGTTT 134
      |||||
Db 3587 TTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATGCT 3528

Qy 135 TTCACCTTTAAACAT 147
      |||||
Db 3527 TTCACCTTTATAT 3515

RESULT 10
US-10-227-195A-1/C
; Sequence 1, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 1030U1
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7175, 7204, 36973, 66372, 76921, 81512, 88727
; OTHER INFORMATION: n = G or C
US-10-227-195A-1

Query Match      12.2%   Score 36.6;   DB 9;   Length 113604;
Best Local Similarity 52.3%;   Pred. No. 41;
Matches 81;   Conservative 0;   Mismatches 74;   Indels 0;   Gaps 0;

Qy 1 TCATTTGCAAGTCAAAATCATCATTAAGTTTGTAGTCTATTAACTGGTTTGTCTAGGTC 60
      |||||
Db 17349 TAACCTGGCTGGTGAATTAATGCATATTTTGTAGTCTTTAACTGACTGGTACATTTT 17290

Qy 61 AGGCATTATTATTACTAACCTTATTGTTAAATTTCTTAACCATAGAATTAACCTAATTAAT 120
      |||||
Db 17289 ATTCACTTTTTTTTACAAATCCCATGATTTGTACACAGATAAAATTTAAATGGCAGAGAAAT 17230

Qy 121 GGTCAATAGAGTTTTTTCACCTTTAACATAGGCCTAT 155
      |||||
Db 17229 TATATATACACTTTTGATATTTATATATGATGT 17195.

RESULT 11
US-10-227-195A-2/C
; Sequence 2, Application US/10227195A
; Publication No. US20030077633A1
; GENERAL INFORMATION:
; APPLICANT: Cox, David
; APPLICANT: Arnold, Deana
```

; TITLE OF INVENTION: Haplotype structure of chromosome 21
; FILE REFERENCE: 103001
; CURRENT APPLICATION NUMBER: US/10/227,195A
; CURRENT FILING DATE: 2002-11-18
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 113604
; TYPE: DNA
; ORGANISM: Human
US-10-227-195A-2

Query Match 12.2%; Score 36.6; DB 9; Length 113604;
Best Local Similarity 52.3%; Pred. No. 41;
Matches 81; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 1 TCATTGCAAGGCAATCATCTATTAGTTTGTAGTCTATTAACTGGGTTTGCTTAGGTC 60
DB 17349 TAACCTGGCTGGATTAAATGATATTTTGTAGTCTTTAACTGACTGCGTACATTTT 17290
QY 61 AGGCATTATTACTAAACCTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAT 120
DB 17289 ATTCACTTTTTCACATCCATGTTGTTACACAGTAATAATTTAAATGSCAGAAAT 17230
QY 121 GGTGATAGAGTTTTCACCTTTTAACTAGGCCTAT 155
DB 17229 TATATATACACTTTTCATATTTATATATATGCGATGT 17195

RESULT 12

US-09-969-373-85
; Sequence 85, Application US/09969373
; Patent No. US20020133852A1

; GENERAL INFORMATION:

; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 85
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-85

Query Match 12.1%; Score 36.4; DB 10; Length 380;
Best Local Similarity 54.5%; Pred. No. 4.1;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 65 ATTATTACTAACTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAATGGTG 124
DB 212 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 271
QY 125 AATAGAGTTTTCACCTTTTAACTAGGCCTATCCCACTGGTGGGATACGACCAATTCGAA 184
DB 272 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 331
QY 185 AGAAAGTCAGTCA 198
DB 332 AGAACATAAATGA 345

RESULT 13

US-09-969-373-86
; Sequence 86, Application US/09969373

; Patent No. US20020133852A1
; GENERAL INFORMATION:
; APPLICANT: Effertz, Roger J.
; APPLICANT: Hauge, Brian M.
; TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
; FILE REFERENCE: 38-10(52679)A
; CURRENT APPLICATION NUMBER: US/09/969,373
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US 09/754,853
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: US 09/760,427
; PRIOR FILING DATE: 2001-01-13
; PRIOR APPLICATION NUMBER: US 09/855,768
; PRIOR FILING DATE: 2001-05-15
; NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 86
; LENGTH: 380
; TYPE: DNA
; ORGANISM: Glycine max
US-09-969-373-86

Query Match 12.1%; Score 36.4; DB 10; Length 380;
Best Local Similarity 54.5%; Pred. No. 4.1;
Matches 73; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

QY 65 ATTATTACTAACTTATTGTTAATATTCTAACCATAAGAAATTAACCTATTAAATGGTG 124
DB 212 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 271
QY 125 AATAGAGTTTTCACCTTTTAACTAGGCCTATCCCACTGGTGGGATACGACCAATTCGAA 184
DB 272 ATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 331
QY 185 AGAAAGTCAGTCA 198
DB 332 AGAACATAAATGA 345

RESULT 14

US-10-239-676-103
; Sequence 103, Application US/10239676
; Publication No. US20030082609A1

; GENERAL INFORMATION:

; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
; FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-04-06
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 228
; SEQ ID NO 103
; LENGTH: 15649
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-103

Query Match

Best Local Similarity 56.8%; Pred. No. 20;
Matches 67; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

